

XX 01-MAY-1998; 98US-00071739.
PR
XX
XX (INSI-) INSIGHT STRATEGY & MARKETING LTD.
PA (HADA-) HADAST MEDICAL RES SERVICES & DEV.
PA (FRIE/) FRIEDMAN M M.
XX
XX Pecker I, Vlodavsky I, Friedmann Y, Perets T;
XX MPI: 2000-052944/04.
DR N-PSDB: AA33290.
XX
XX Heparanase-specific molecular probes useful for diagnosis and treatment,
PT e.g. of tumors, and for targeted drug delivery.
XX
XX Example: Page 81-82; 90pp; English.
XX
CC The present invention describes heparanase-specific molecular probes,
CC useful for methods of detecting heparanase in situ. The probes and anti-
CC heparanase antibodies are used to detect or quantify the expression of
CC heparanase, for diagnosis and monitoring of diseases (especially
CC metastasis), for treatment of heparanase-associated diseases (e.g.
CC tumors, (adeno)carcinoma, squamous cell carcinoma, teratocarcinoma,
CC mesothelioma, melanoma, lymphoma or leukemia, a solid cancer (or its
CC metastases) derived from liver, prostate, bladder, breast, ovary, cervix,
CC colon, skin, intestine, stomach, uterus and pancreas, kidney disease,
CC diabetes and inflammation, haemorrhagic nephritis, nephrotic syndrome,
CC sepsis and inflammatory or autoimmune disease), for targeted drug
CC delivery (e.g. of anticancer agents) and as research reagents. The
CC present sequence represents human heparanase, which is used in the
CC exemplification of the present invention
XX
SQ Sequence 543 AA;

Query Match 99.9%; Score 2838; DB 3; Length 543;

Best Local Similarity 99.8%; Pred. No. 5.3e-275;

Matches 542; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLTRKSPALPPMLLLGPGALPRPAQADVVLDLFTQEPHLTVSPFLSYT 60
DB 1 MLTRKSPALPPMLLLGPGALPRPAQADVVLDLFTQEPHLTVSPFLSYT 60
QY 61 IDANLATDERFLILGSPRLTARGSPAYLRFQGTXTDFLIFDPKKESTFEERSYQS 120
DB 61 IDANLATDERFLILGSPRLTARGSPAYLRFQGTXTDFLIFDPKKESTFEERSYQS 120
QY 121 QVNODICKYGSIPDPVEEKLRLWEPYQEQLLREHYQKKFNSTYSRSSVDVLYTFANCS 180
DB 121 QVNODICKYGSIPDPVEEKLRLWEPYQEQLLREHYQKKFNSTYSRSSVDVLYTFANCS 180
QY 181 GLDLIFGLNALRTADLQWSSNAQLLDYCSSKGYNISWEIGNEPNSFLKKADIFINGS 240
DB 181 GLDLIFGLNALRTADLQWSSNAQLLDYCSSKGYNISWEIGNEPNSFLKKADIFINGS 240
QY 241 QGGEDEFIQHLKLLRKSTFNKAKLYGPVQGPRTAKMLKSFLLKAGGEVIDSVTWHYYL 300
DB 241 QGGEDEYIQHLKLLRKSTFNKAKLYGPVQGPRTAKMLKSFLLKAGGEVIDSVTWHYYL 300
QY 301 NGRTATREDFLNPVDVLDIFISSVQKVFQVVESTPRGKXWLGETSAYGGAPLLSDTPA 360
DB 301 NGRTATREDFLNPVDVLDIFISSVQKVFQVVESTPRGKXWLGETSAYGGAPLLSDTPA 360
QY 361 AGFMWLDKGLSARMGIEVVMROVFFGAGNYHLVDENFPLPDYWLSTLFFKLVGTKVLM 420
DB 361 AGFMWLDKGLSARMGIEVVMROVFFGAGNYHLVDENFPLPDYWLSTLFFKLVGTKVLM 420
QY 421 ASVGSSKRRRLRVYLHCTNTDNPXYKEGDLTYAINLHNVTKYRLPYPPSNKQVDKYL 480
DB 421 ASVGSSKRRRLRVYLHCTNTDNPXYKEGDLTYAINLHNVTKYRLPYPPSNKQVDKYL 480
QY 481 RPLGPHGLSKSVQNLGLTKAVDDQTLPLMEKPLRPSSSLGLPAFSYSFVIRAKYA 540
DB 481 RPLGPHGLSKSVQNLGLTKAVDDQTLPLMEKPLRPSSSLGLPAFSYSFVIRAKYA 540

QY 541 ACT 543
DB 541 ACT 543

Search completed: March 23, 2005, 11:25:49
Job time : 114.5 secs

Db 301 NGRTATREDFLNPVDLDFISSVQKVFQVVESTRGKVMLGETSAYGGAPLLSDTFA 360
 QY 361 AGFMWLDKLGISARMGIEVVMKQVFAGNHYLVDENDPLPDYMLSLFFKLVGTXYLM 420
 Db 361 AGFMWLDKLGISARMGIEVVMKQVFAGNHYLVDENDPLPDYMLSLFFKLVGTXYLM 420
 QY 421 ASVQSGSKRRKRLVYVLAHCTNTDNPARYKEGDLTYALNLHVTKYLRLPYFSNKOVDKYL 480
 Db 421 ASVQSGSKRRKRLVYVLAHCTNTDNPARYKEGDLTYALNLHVTKYLRLPYFSNKOVDKYL 480
 QY 481 RPLGPHGLLSKSVQNLGLTLKAVDDOTLPPLMEKPLRPSSSLGLPAFSYSPFVIRNAKVA 540
 Db 481 RPLGPHGLLSKSVQNLGLTLKAVDDOTLPPLMEKPLRPSSSLGLPAFSYSPFVIRNAKVA 540
 QY 541 ACT 543
 Db 541 ACT 543

RESULT 14

AAB08849
 ID AAB08849 standard; protein; 543 AA.

AC AAB08849;

DT 15-JAN-2001 (first entry)

DE Amino acid sequence of a human heparanase polypeptide.

XX Human; heparanase; gene therapy; tumour; inflammation; autoimmunity;

KW heparin-binding growth factor; cytokine; neurodegenerative plaque;

KW wound healing; infection; burn; angiogenesis; restenosis;

KW atherosclerosis; inflammation; neurodegenerative disease;

KW Gersmann-Strauszler Syndrome; Creutzfeldt-Jakob disease.

XX Homo sapiens.

PN WO200052178-A1.

PD 08-SEP-2000.

PF 14-FEB-2000; 2000MO-US003542.

PR 01-MAR-1999; 99US-00258892.

PA (INSI-) INSIGHT STRATEGY & MARKETING LTD.

PA (HADA-) HADASIT MEDICAL RES SERVICES & DEV.

PA (FRIE/) FRIEDMAN M M.

PI Pecker I, Vlodaevsky I, Feinstein E;

XX WPI; 2000-579289/54.

DR N-PSDB; AAA75051.

XX New polynucleotides encoding a polypeptide having heparanase activity,

PT useful in wound healing and in gene therapy, particularly in treating

PT tumor, inflammation, autoimmunity, neurodegenerative diseases.

XX Claim 22; Fig 1; 152pp; English.

XX The present sequence represents a human protein with heparanase catalytic

CC activity. The heparanase (hpa) polynucleotide is useful in gene therapy,

CC particularly in treating tumour, inflammation or autoimmunity.

CC Particularly, the polynucleotide is useful in modulating the

CC bioavailability of heparin-binding growth factors, cellular responses to

CC heparin-binding growth factors (e.g. bFGF) and cytokines (e.g.

CC bacterial or protozoa infections
 XX
 SQ Sequence 543 AA;
 Query Match 99.9%; Score 2838; DB 3; Length 543;
 Best Local Similarity 99.8%; Pred. No. 5.3e-275;
 Matches 542; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MLNSKSPALPPPLMLLLPLGLPLSPGALPPPAQADVDLDFFTOEPLHVSPLSVT 60
 Db 1 MLNSKSPALPPPLMLLLPLGLPLSPGALPPPAQADVDLDFFTOEPLHVSPLSVT 60
 QY 61 IDANLATDPPRFLILGSPKRLTLARGLSPALTRGGCTTDPDLIDPKKESFEEERSYQWS 120
 Db 61 IDANLATDPPRFLILGSPKRLTLARGLSPALTRGGCTTDPDLIDPKKESFEEERSYQWS 120
 QY 121 QVNODICKYGSIPPVVEKRLLEMPYQQLLREHYQKFKFNSTYSRSSVDVLTAFNCS 180
 Db 121 QVNODICKYGSIPPVVEKRLLEMPYQQLLREHYQKFKFNSTYSRSSVDVLTAFNCS 180
 QY 181 GDLIFGLNALRLRTADLQNSSNAQLLDYCSSKGYNISWEIGNEPNSFLKKADIFINGS 240
 Db 181 GDLIFGLNALRLRTADLQNSSNAQLLDYCSSKGYNISWEIGNEPNSFLKKADIFINGS 240
 QY 241 QLGEDPIQLHKLLRSTFRNAKLYGPDYGOBRKTAKMLXSLFKAEGEVIDSVTHHYLL 300
 Db 241 QLGEDPIQLHKLLRSTFRNAKLYGPDYGOBRKTAKMLXSLFKAEGEVIDSVTHHYLL 300
 QY 301 NGRTATREDFLNPVDLDFISSVQKVFQVVESTRGKVMLGETSAYGGAPLLSDTFA 360
 Db 301 NGRTATREDFLNPVDLDFISSVQKVFQVVESTRGKVMLGETSAYGGAPLLSDTFA 360
 QY 361 AGFMWLDKLGISARMGIEVVMKQVFAGNHYLVDENDPLPDYMLSLFFKLVGTXYLM 420
 Db 361 AGFMWLDKLGISARMGIEVVMKQVFAGNHYLVDENDPLPDYMLSLFFKLVGTXYLM 420
 QY 421 ASVQSGSKRRKRLVYVLAHCTNTDNPARYKEGDLTYALNLHVTKYLRLPYFSNKOVDKYL 480
 Db 421 ASVQSGSKRRKRLVYVLAHCTNTDNPARYKEGDLTYALNLHVTKYLRLPYFSNKOVDKYL 480
 QY 481 RPLGPHGLLSKSVQNLGLTLKAVDDOTLPPLMEKPLRPSSSLGLPAFSYSPFVIRNAKVA 540
 Db 481 RPLGPHGLLSKSVQNLGLTLKAVDDOTLPPLMEKPLRPSSSLGLPAFSYSPFVIRNAKVA 540
 QY 541 ACT 543
 Db 541 ACT 543
 RESULT 15
 ID AAY52990 standard; protein; 543 AA.
 XX AAY52990;
 AC AAY52990;
 XX 21-FEB-2000 (first entry)
 DT Human heparanase protein sequence.
 DE
 XX Human; heparanase; hpa; diagnosis; therapy; tumour; cytostatic;
 KW antidiabetic; immunomodulatory; anti-inflammatory; nephrotropic;
 KW metastasis; adenocarcinoma; squamous cell carcinoma; teratocarcinoma;
 KW mesothelioma; melanoma; lymphoma; leukemia; cancer; sepsis; diabetes;
 KW inflammation; haemorrhagic nephritis; nephrotic syndrome;
 KW autoimmune disease; anticancer; kidney disease.
 XX Homo sapiens.
 OS WO957153-A1.
 PN 11-NOV-1999.
 PD 29-APR-1999; 99MO-US009255.

CC disintegration of neurodegenerative plaques. Heparanase may be useful for
 CC conditions such as wound healing, angiogenesis, restenosis, and viral
 CC atherosclerosis, inflammation, neurodegenerative diseases, and viral
 CC infections. Mammalian heparanase can be used to neutralize plasma
 CC heparin, and anti-heparanase antibodies may be applied for
 CC immunodetection and diagnosis of micrometastases, autoimmune lesions, and
 CC renal failure in biopsy specimens, plasma samples, and body fluids. The
 CC present sequence represents human heparanase

XX Sequence 543 AA;

Query Match 99.9%; Score 2838; DB 2; Length 543;

Best Local Similarity 99.8%; Pred. No. 5.3e-275;

Matches 542; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLRSKRALPPMLMLLLGPGPLSPGALPRPAQADVVDDLFQOEPLHLVSPFLSVT 60
 DB 1 MLRSKRALPPMLMLLLGPGPLSPGALPRPAQADVVDDLFQOEPLHLVSPFLSVT 60
 QY 61 IDANLATPPRFLILGSPKRLTARGLSPAYLRFPGTKTDPLFPDKKESTFEERSYMQS 120
 DB 61 IDANLATPPRFLILGSPKRLTARGLSPAYLRFPGTKTDPLFPDKKESTFEERSYMQS 120
 QY 121 QVNODICKYGSIPDPVEEKLRLMPYOEQLLREHYOKKFNKSTYSRSSVDVLYTFANCS 180
 DB 121 QVNODICKYGSIPDPVEEKLRLMPYOEQLLREHYOKKFNKSTYSRSSVDVLYTFANCS 180
 QY 121 QVNODICKYGSIPDPVEEKLRLMPYOEQLLREHYOKKFNKSTYSRSSVDVLYTFANCS 180
 DB 121 QVNODICKYGSIPDPVEEKLRLMPYOEQLLREHYOKKFNKSTYSRSSVDVLYTFANCS 180
 QY 181 GLDLIFGNALLRTADLQWNSNAQLLDYCSSKKNYSWEIGNEPNSTLKKADIFINCS 240
 DB 181 GLDLIFGNALLRTADLQWNSNAQLLDYCSSKKNYSWEIGNEPNSTLKKADIFINCS 240
 QY 241 QLGEDFIQLHKLRLKSTFKNAKLYGPDVGQPRKTKAKMLKSLKAGGEYIDSVTMHHYYL 300
 DB 241 QLGEDFIQLHKLRLKSTFKNAKLYGPDVGQPRKTKAKMLKSLKAGGEYIDSVTMHHYYL 300
 QY 301 NGRTATREDPLNPVDLDFISSVQKVFQVVESTTRPGKKVWLGETSSAYGAGAPLLSDTFA 360
 DB 301 NGRTATREDPLNPVDLDFISSVQKVFQVVESTTRPGKKVWLGETSSAYGAGAPLLSDTFA 360
 QY 301 NGRTATREDPLNPVDLDFISSVQKVFQVVESTTRPGKKVWLGETSSAYGAGAPLLSDTFA 360
 DB 301 NGRTATREDPLNPVDLDFISSVQKVFQVVESTTRPGKKVWLGETSSAYGAGAPLLSDTFA 360
 QY 361 AGFMWLDKGLSARNGIIVMQRQVFFGAGNYHLVDENPDPLDVMYLSLFFKLVGTGYLVM 420
 DB 361 AGFMWLDKGLSARNGIIVMQRQVFFGAGNYHLVDENPDPLDVMYLSLFFKLVGTGYLVM 420
 QY 421 ASVQSKRRKRLRVLYHCTNTDNPRIKESGDLTYALNLHNTVTKYLRPFPSNKQVDKYL 480
 DB 421 ASVQSKRRKRLRVLYHCTNTDNPRIKESGDLTYALNLHNTVTKYLRPFPSNKQVDKYL 480
 QY 481 RPLGPHGLLSKSVQNLGLTLKQVDDQTLPLMEKPLRPSSSLGLPAFSYSFVIRNAKVA 540
 DB 481 RPLGPHGLLSKSVQNLGLTLKQVDDQTLPLMEKPLRPSSSLGLPAFSYSFVIRNAKVA 540
 QY 541 ACI 543
 DB 541 ACI 543

RESULT 13
 AA57590
 AA57590 standard; protein; 543 AA.

XX AA57590;

DT 02-MAR-2000 (first entry)

XX Human heparanase.

KW Human; heparanase; hpa; genetic modification; expression; anticancer;
 KW angiogenesis; anti-angiogenic; antiproliferative; antiviral; antitumor;
 KW anti-atherosclerotic; anti-inflammatory; antineurodegeneration;
 KW heparan sulphate; heparin-binding growth factor; tumor angiogenesis;
 KW metastasis; wound healing; restenosis; atherosclerosis; inflammation;
 KW neurodegeneration; viral infection; cystic fibrosis; cancer; diagnosis;
 KW micrometastasis; autoimmune lesion; kidney failure.

XX Homo sapiens.
 OS
 XX MO9957244-AL.
 PN
 XX 11-NOV-1999.
 PD
 XX 29-APR-1999; 99WO-US009256.
 PF
 XX 01-MAY-1998; 98US-00071618.
 PR
 XX 02-MAR-1999; 99US-00260038.
 PA
 XX (INSI-) INSIGHT STRATEGY & MARKETING LTD.
 PA (FRIE/) FRIEDMAN M M.
 XX
 PI Ben-Artzi H, Ayal-Hershenkowitz M, Yacoby-Zeevi O, Pecker I;
 PI Peleg Y, Shlomi Y;
 XX
 DR MPI, 2000-062144/05.
 DR N-PSDB; AA239195.
 XX
 PT Engineered cells that express recombinant heparanase, useful
 PT therapeutically, e.g. for treating angiogenesis and to screen for
 PT specific inhibitors, potential anticancer agents.
 PS
 XX Claim 3; Page 107-109; 118pp; English.

The present invention describes genetically modified cells (A) containing
 a polynucleotide (I) that encodes a polypeptide with heparanase activity,
 and expresses recombinant heparanase (II). Heparanase cleaves heparan
 sulphate (HS) at specific intrachain sites, resulting in release of
 heparin-binding growth factors, enzymes and proteins that are sequestered
 by HS in basement membranes, extracellular matrix or cell surfaces. It
 may also be implicated in tumor angiogenesis and metastases. (II) is
 potentially useful in wound healing and for treating angiogenesis,
 restenosis, atherosclerosis, inflammation, neurodegeneration, viral
 infection and cystic fibrosis. It can also be used to neutralise heparin
 (an alternative to protamine) and to screen for specific inhibitors
 (potentially useful for treating cancer and metastases). Antibodies
 raised against (II) are used for immunodetection and diagnosis of
 micrometastases, autoimmune lesions and kidney failure. (A) provide (II)
 in large quantities, in a form that is homogeneously processed and
 activated/neutralised by a dedicated protease. The present sequence
 represents human heparanase

Sequence 543 AA;

Query Match 99.9%; Score 2838; DB 3; Length 543;
 Best Local Similarity 99.8%; Pred. No. 5.3e-275;
 Matches 542; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLRSKRALPPMLMLLLGPGPLSPGALPRPAQADVVDDLFQOEPLHLVSPFLSVT 60
 DB 1 MLRSKRALPPMLMLLLGPGPLSPGALPRPAQADVVDDLFQOEPLHLVSPFLSVT 60
 QY 61 IDANLATPPRFLILGSPKRLTARGLSPAYLRFPGTKTDPLFPDKKESTFEERSYMQS 120
 DB 61 IDANLATPPRFLILGSPKRLTARGLSPAYLRFPGTKTDPLFPDKKESTFEERSYMQS 120
 QY 121 QVNODICKYGSIPDPVEEKLRLMPYOEQLLREHYOKKFNKSTYSRSSVDVLYTFANCS 180
 DB 121 QVNODICKYGSIPDPVEEKLRLMPYOEQLLREHYOKKFNKSTYSRSSVDVLYTFANCS 180
 QY 181 GLDLIFGNALLRTADLQWNSNAQLLDYCSSKKNYSWEIGNEPNSTLKKADIFINCS 240
 DB 181 GLDLIFGNALLRTADLQWNSNAQLLDYCSSKKNYSWEIGNEPNSTLKKADIFINCS 240
 QY 241 QLGEDFIQLHKLRLKSTFKNAKLYGPDVGQPRKTKAKMLKSLKAGGEYIDSVTMHHYYL 300
 DB 241 QLGEDFIQLHKLRLKSTFKNAKLYGPDVGQPRKTKAKMLKSLKAGGEYIDSVTMHHYYL 300
 QY 301 NGRTATREDPLNPVDLDFISSVQKVFQVVESTTRPGKKVWLGETSSAYGAGAPLLSDTFA 360
 DB 301 NGRTATREDPLNPVDLDFISSVQKVFQVVESTTRPGKKVWLGETSSAYGAGAPLLSDTFA 360

DT 20-MAR-2003 (revised)
 DT 14-OCT-1999 (first entry)
 XX A human protein with heparanase activity.
 DE Human; heparanase; heparan sulfate; trauma; autoimmune disease;
 KW skin disease; cardiovascular disease; nervous system disease;
 KW Alzheimer's disease; cancer; cancer metastasis; angiogenesis;
 KW inflammation; arthritis.
 XX Homo sapiens.
 OS
 XX WO9940207-A1.
 XX
 XX 12-AUG-1999.
 XX
 XX 05-FEB-1999; 99WO-EP000777.
 XX
 XX 09-FEB-1998; 98GB-00002725.
 XX
 XX (NOVS) NOVARTIS AG.
 XX (NOVS) NOVARTIS-ERFINDUNGEN VERW GES MBH.
 XX Nakajima M, Toyoshima M;
 XX WPI; 1999-494300/41.
 XX N-PSDB; AAX86671.
 XX
 XX New heparanase polypeptide useful for treating autoimmune diseases, skin
 PT diseases, cardiovascular diseases and nervous system diseases including
 PT Alzheimer's disease.
 XX
 XX Claim 3; Page 29-31; 40pp; English.
 XX
 XX The present sequence represents a polypeptide with human heparanase
 CC biological activity. Antagonists and inhibitors of the protein prevent it
 CC from degrading the extracellular matrix and releasing heparan sulfate
 CC from the extracellular matrix surface. The heparanase protein or the anti-
 CC heparanase antibody are used in pharmaceutical compositions for treating
 CC warm blooded animals suffering from a disease resulting from shortage or
 CC lack of the heparanase protein, or from excessive activity or over-
 CC expression of the heparanase protein, respectively. The heparanase
 CC protein is used in treating diseases such as trauma, autoimmune disease,
 CC skin diseases, cardiovascular diseases and nervous system diseases
 CC including Alzheimer's disease resulting from shortage or lack of
 CC polypeptide. The anti-heparanase antibody is used in treating the
 CC diseases like cancer, cancer metastasis, angiogenesis and inflammation
 CC including arthritis resulting from excessive activity or over expression
 CC of heparanase protein. The anti-heparanase antibody can be used to detect
 CC the presence or absence of polypeptide and its concentration. (Updated on
 CC 20-MAR-2003 to correct PA field.)
 CC
 XX Sequence 588 AA;
 SQ
 Query Match 100.0%; Score 2841; DB 2; Length 588;
 Best Local Similarity 100.0%; Pred. No. 3e-275;
 Matches 543; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 241 QLGEDPTQLHKLRKSPFNKAKLYGPVCGPRRKATKMLKSLKAGGEVIDSVTWHRYYL 300
 DB 286 QLGEDPTQLHKLRKSTFPNKKLYGPDVQPRKRTAKMLKSLKAGGEVIDSVTWHRYYL 345
 OY 301 NGRATREDFLNPVDVDFISSVQKVFQVESYTRPGKRWLGETSSAYGGGAPLLSDTFA 360
 DB 346 NGRATREDFLNPVDVDFISSVQKVFQVESYTRPGKRWLGETSSAYGGGAPLLSDTFA 405
 OY 361 AGFWMLDKLGLSARMGEVVMRQVFFGAGNYHLVDENFDPDLPYWLSTLFFKLVGTQVLM 420
 DB 406 AGFWMLDKLGLSARMGEVVMRQVFFGAGNYHLVDENFDPDLPYWLSTLFFKLVGTQVLM 465
 OY 421 ASVQSKRRKRLRYVLIHCTNTDNPYKGGDLTLVAINLHNTKYLRLPYPSNKQVDKTYL 480
 DB 466 ASVQSKRRKRLRYVLIHCTNTDNPYKGGDLTLVAINLHNTKYLRLPYPSNKQVDKTYL 525
 OY 481 RPLGPHGLSKSVQNLGLTKMVDQTLPLMEKPLRPGSSGLPAPSYSPFVLRNKA 540
 DB 526 RPLGPHGLSKSVQNLGLTKMVDQTLPLMEKPLRPGSSGLPAPSYSPFVLRNKA 585
 OY 541 ACI 543
 DB 586 ACI 588

RESULT 12
 AAY02345
 ID AAY02345 standard; protein; 543 AA.
 XX
 XX AAY02345;
 XX
 XX 09-JUL-1999 (first entry)
 DT
 XX
 DE A human heparanase protein.
 XX
 XX Heparanase; hp; modulator; heparin-binding growth factor;
 KW cellular response; cytokine; cell interaction; plasma lipoprotein;
 KW cellular susceptibility; infection; disintegration;
 KW neurodegenerative plaque; wound healing; angiogenesis; restenosis;
 KW atherosclerosis; inflammation; neurodegenerative disease; neutralise;
 KW plasma heparin; micrometastasis; autoimmune lesion; renal failure.
 XX
 XX Homo sapiens.
 OS
 XX WO9911798-A1.
 XX
 XX 11-MAR-1999.
 XX
 XX 31-AUG-1998; 98WO-US017954.
 XX
 XX 02-SEP-1997; 97US-00922170.
 XX
 XX 02-JUL-1998; 98US-00109386.
 XX
 XX (INST-) INSTIGT STRATEGY & MARKETING LTD.
 XX (HADA-) HADASTI MEDICAL RES SERVICES & DEV.
 XX (FRIE/) FRIEDMAN M M.
 XX
 XX Pecker I, Vlodayevy I, Feinstein E;
 XX WPI; 1999-302255/25.
 XX N-PSDB; AAX35648.
 XX
 XX New human polynucleotide useful for treating angiogenesis, restenosis,
 PT and inflammation.
 PT
 XX
 PS Claim 6; Fig 1; 63pp; English.
 XX
 CC The specification describes a polypeptide having heparanase (hp)
 CC activity. The recombinant protein is used as a modulator of heparin-
 CC binding growth factors, cellular responses to heparin-binding growth
 CC factors and cytokines, cell interaction with plasma lipoproteins,
 CC cellular susceptibility to viral, protozoal and bacterial infections or

QY 241 QLGEDFIQLHLKLRKSTFNNAKLYGPDVGQPRKRTAKMLKSFKAAGGEVIDSVTHHHYLL 300
 DB 241 QLGEDFIQLHLKLRKSTFNNAKLYGPDVGQPRKRTAKMLKSFKAAGGEVIDSVTHHHYLL 300
 QY 301 NGRTATREDPFLNPDVLDIFISSVQKVFQVVESTPRGKRWLGETSAYGGAPLLSDTPA 360
 DB 301 NGRTATREDPFLNPDVLDIFISSVQKVFQVVESTPRGKRWLGETSAYGGAPLLSDTPA 360
 QY 361 AGFMMLDKLGLSARMGIEVVMROVFFGAGNYHLVDENPDLDPYWLSTLFFKLVGKTVLM 420
 DB 361 AGFMMLDKLGLSARMGIEVVMROVFFGAGNYHLVDENPDLDPYWLSTLFFKLVGKTVLM 420
 QY 421 ASVQSKRRKRLRVYLHCTNTDNPXYKEGDLTYAINHVTYKRLRPPYFSNKQVDKYL 480
 DB 421 ASVQSKRRKRLRVYLHCTNTDNPXYKEGDLTYAINHVTYKRLRPPYFSNKQVDKYL 480
 QY 481 RPLGPHGLSKSVQNLGLTLKRVDDQTLPLMEKPLRPSSIGLPAFSYSPFVIRNAKVA 540
 DB 481 RPLGPHGLSKSVQNLGLTLKRVDDQTLPLMEKPLRPSSIGLPAFSYSPFVIRNAKVA 540
 QY 541 ACT 543
 DB 541 ACT 543

RESULT 10

ADP25079
 ADP25079 standard; protein; 543 AA.

AC ADP25079;
 DT 18-NOV-2004 (first entry)

DE PRO polypeptide SEQ ID NO:2257.

KM PRO; antiinflammatory; antiarthritic; antirheumatic; immunosuppressive;
 KM osteopathic; antidiabetic; dermatological; antipsoriatic; antiallergic;
 KM antiasmastic; hepatotropic; respiratory; gene therapy; immune system.
 OS Unidentified.

PN WO2004041170-A2.

PD 21-MAY-2004.

PF 30-OCT-2003; 2003WO-US034312.

PR 01-NOV-2002; 2002US-0423394P.

PA (GETH) GENENTECH INC.

PI Clack H, Scheenfeld J, Van Lookeren M, Williams PM, Wood WI;
 PI Wu TD;

DR WPI: 2004-419628/39.

DR N-PSDB; ADP25078.

PT New PRO polypeptides and polynucleotides, useful for treating e.g.
 PT erythematous, rheumatoid arthritis, diabetes mellitus, immune-mediated
 PT renal disease, or demyelinating diseases of the central or peripheral
 PT nervous system.

PS Claim 7; SEQ ID NO 2257; 2940bp; English.

XX The invention relates to a novel isolated nucleic acid and the PRO
 XX polypeptide encoded by it. A protein of the invention has
 XX antiinflammatory, antiarthritic, antirheumatic, immunosuppressive,
 XX osteopathic, antidiabetic, dermatological, antipsoriatic, antiallergic,
 XX antiasmastic, hepatotropic, and respiratory activity. A polynucleotide
 CC of the invention may have a use in gene therapy. The PRO polypeptide, its
 CC agonist, antagonist, or antibody that specifically binds to the
 CC polypeptide is useful for treating an immune related disorder such as

CC systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis,
 CC juvenile chronic arthritis, a spondyloarthropathy, systemic sclerosis, an
 CC idiopathic inflammatory myopathy, Sjogren's syndrome, systemic
 CC vasculitis, sarcoidosis, autoimmune haemolytic anaemia, autoimmune
 CC thrombocytopenia, thyroditis, diabetes mellitus, immune-mediated renal
 CC disease, a demyelinating disease of the central or peripheral nervous
 CC system, idiopathic demyelinating polyneuropathy, Guillain-Barre syndrome,
 CC a chronic inflammatory demyelinating polyneuropathy, a hepatobiliary
 CC disease, infectious or autoimmune chronic active hepatitis, primary
 CC biliary cirrhosis or autoimmune hepatitis, sclerosing cholangitis,
 CC inflammatory bowel disease, gluten-sensitive enteropathy, Whipple's
 CC disease, an autoimmune or immune-mediated skin disease, a bullous skin
 CC disease, erythema multiforme, contact dermatitis, psoriasis, an allergic
 CC disease, asthma, allergic rhinitis, atopic dermatitis, food
 CC hypersensitivity, urticaria, an immunologic disease of the lung,
 CC eosinophilic pneumonia, idiopathic pulmonary fibrosis, hypersensitivity
 CC pneumonitis, a transplantation associated disease, graft rejection or
 CC graft-versus-host disease. The present sequence represents a PRO protein
 CC of the invention.

CC Sequence 543 AA;

Query Match 100.0%; Score 2841; DB 8; Length 543;

Best Local Similarity 100.0%; Pred. No. 2.7e-275;

Matches 543; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLRSKPALPPMLMLLLGLPLSPGALPPRAQADVVLDLDFTEPHLVSPSLSYT 60
 DB 1 MLRSKPALPPMLMLLLGLPLSPGALPPRAQADVVLDLDFTEPHLVSPSLSYT 60
 QY 61 IDANLATDPRFLILGSPKRLTARGLSPAYLRFQGTKTDFLIIDPKKSTFEERSYMQS 120
 DB 61 IDANLATDPRFLILGSPKRLTARGLSPAYLRFQGTKTDFLIIDPKKSTFEERSYMQS 120
 QY 121 QVNODICKGSIIPDVEEKLRLIEWPYQEQLLREHYQKKFKNSTYSRSSVDVLYTANCS 180
 DB 121 QVNODICKGSIIPDVEEKLRLIEWPYQEQLLREHYQKKFKNSTYSRSSVDVLYTANCS 180
 QY 181 GDDLIFGLNALRTADLQWNSNAQLLDYCSSKGYNISMEIGNEBNSFLKADIFINGS 240
 DB 181 GDDLIFGLNALRTADLQWNSNAQLLDYCSSKGYNISMEIGNEBNSFLKADIFINGS 240
 QY 241 QLGEDFIQLHLKLRKSTFNNAKLYGPDVGQPRKRTAKMLKSFKAAGGEVIDSVTHHHYLL 300
 DB 241 QLGEDFIQLHLKLRKSTFNNAKLYGPDVGQPRKRTAKMLKSFKAAGGEVIDSVTHHHYLL 300
 QY 301 NGRTATREDPFLNPDVLDIFISSVQKVFQVVESTPRGKRWLGETSAYGGAPLLSDTPA 360
 DB 301 NGRTATREDPFLNPDVLDIFISSVQKVFQVVESTPRGKRWLGETSAYGGAPLLSDTPA 360
 QY 361 AGFMMLDKLGLSARMGIEVVMROVFFGAGNYHLVDENPDLDPYWLSTLFFKLVGKTVLM 420
 DB 361 AGFMMLDKLGLSARMGIEVVMROVFFGAGNYHLVDENPDLDPYWLSTLFFKLVGKTVLM 420
 QY 421 ASVQSKRRKRLRVYLHCTNTDNPXYKEGDLTYAINHVTYKRLRPPYFSNKQVDKYL 480
 DB 421 ASVQSKRRKRLRVYLHCTNTDNPXYKEGDLTYAINHVTYKRLRPPYFSNKQVDKYL 480
 QY 481 RPLGPHGLSKSVQNLGLTLKRVDDQTLPLMEKPLRPSSIGLPAFSYSPFVIRNAKVA 540
 DB 481 RPLGPHGLSKSVQNLGLTLKRVDDQTLPLMEKPLRPSSIGLPAFSYSPFVIRNAKVA 540
 QY 541 ACT 543
 DB 541 ACT 543

RESULT 11
 AAY30124
 ID AAY30124 standard; protein; 588 AA.
 XX AAY30124;
 AC
 XX

```

QY 481 RPLGPHGLSKSVOLNGTLTKWVDOTLPPLMEKPLRPGSSGLPAPSYSPFVIRNAKYA 540
DB 481 RPLGPHGLSKSVOLNGTLTKWVDOTLPPLMEKPLRPGSSGLPAPSYSPFVIRNAKYA 540
QY 541 ACT 543
DB 541 ACT 543

RESULT 9
ADR88210
ID ADR88210 standard; protein; 543 AA.
AC ADR88210;
XX 18-NOV-2004 (first entry)
DT 18-NOV-2004 (first entry)
DE Human preproheparanase.
XX
XX Targeted drug delivery; inflammatory disorder; wound; scar; vasculopathy;
XX autoimmune disorder; cancer; angiogenesis; metastatic disease;
XX atherosclerosis; aneurysm; solid cancer; non-solid cancer;
XX haematopoietic malignancy; lymphocytic leukaemia; myelogenous leukaemia;
XX Hodgkin's disease; multiple myeloma; haemangiosarcoma; Kaposi's sarcoma;
XX human; heparanase; enzyme.
XX
XX Homo sapiens.
XX
XX Key
XX Peptide
XX 1. .35
XX /label= Signal_peptide
XX 36. .543
XX /label= Mature_heparanase
XX 36. .109
XX /note= "8 kDa subunit of mature heparanase dimer"
XX 89. .107
XX /note= Functional peptide epitope
XX 158. .543
XX /note= "45 kDa subunit of mature heparanase dimer"
XX 219. .233
XX /note= Functional peptide epitope
XX 225
XX /note= "Active site residue"
XX 258. .266
XX /note= "Putative heparin binding domain"
XX 294. .307
XX /note= Functional peptide epitope
XX 334. .348
XX /note= Functional peptide epitope
XX 343
XX /note= "Active site residue"
XX 414. .420
XX /note= "Putative heparin binding domain"
XX 437. .446
XX /note= Functional peptide epitope
XX
XX Domain
XX
XX US2004170631-A1.
XX
XX 02-SEP-2004.
XX
XX 28-NOV-2003; 2003US-00722502.
XX
XX 02-SEP-1997; 97US-00922170.
XX 01-MAY-1998; 98US-00071739.
XX 04-NOV-1998; 98US-00186200.
XX 19-FEB-2003; 2003US-00368044.
XX 22-AUG-2003; 2003US-00645659.
XX
XX (YACOBY) YACOBY-ZEEVI O.
XX (PEREZ) PEREZ T.
XX (MIRON) MIRON D.
XX (SHLO) SHLOMI Y.
XX (PECKER) PECKER I.

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PA (AYAL/) AYAL-HERSHKOVITZ M.
PA (FEIN/) FEINSTEIN E.
PA (VGH/) VAN GELDER J M.
PA (VLAD/) VLADAVSKY I.
PA (FRIE/) FRIEDMANN Y.
XX
XX Yacoby-Zeevi O, Perez T, Miron D, Shlomi Y, Pecker I;
XX Ayal-Hershkovitz M, Feinstein E, Van Gelder JM, Vladavsky I;
XX Friedmann Y;
XX
XX WPI; 2004-625084/60.
XX
XX
XX Claim 2; SEQ ID NO 4; 58pp; English.
XX
XX The invention relates to a method of targeted drug delivery to a tissue
XX of a patient, the tissue expressing heparanase. The method comprises
XX providing a complex of a drug directly or indirectly linked to an anti-
XX heparanase antibody, and administering the complex to the patient. In the
XX targeted drug delivery, the antibody comprises an antibody or its portion
XX capable of specifically binding to at least one epitope of a heparanase
XX protein. The composition and methods of the invention are useful for
XX diagnosing, preventing or treating conditions associated with heparanase
XX catalytic activity (e.g. an inflammatory disorder, wound, scar,
XX vasculopathy, an autoimmune disorder, cancer, angiogenesis, cell
XX proliferation, invasion of circulating tumour cells and metastatic
XX disease), for purifying heparanase, or for developing drugs for those
XX heparanase-associated conditions. The vasculopathy is atherosclerosis,
XX restenosis or aneurysm. The cancerous condition is a solid cancer or a
XX non-solid cancer. The non-solid cancer is a haematopoietic malignancy
XX selected from acute lymphocytic leukaemia (ALL), acute myelogenous
XX leukaemia, chronic lymphocytic leukaemia (CLL), chronic myelogenous
XX leukaemia (CMML), myelodysplastic syndrome (MDS), mast cell leukaemia,
XX Hodgkin's disease, non-Hodgkin's lymphomas, Burkitt's lymphoma and
XX multiple myeloma. The solid cancer is selected from tumours in lip and
XX oral cavity, pharynx, larynx, paranasal sinuses, major salivary glands,
XX thyroid gland, oesophagus, stomach, small intestine, colon, colorectum,
XX anal canal, liver, gallbladder, extrahepatic bile ducts, ampulla of
XX Vater, exocrine pancreas, lung, pleural mesothelioma, soft tissue
XX sarcoma, carcinoma and malignant melanoma of the skin, breast, vulva,
XX vagina, cervix uteri, ovary, fallopian tube, gestational trophoblastic
XX tumours, penis, prostate, testis, kidney, renal pelvis, ureter, urinary
XX bladder, urethra, carcinoma of the eyelid, carcinoma of the conjunctiva,
XX malignant melanoma of the conjunctiva, malignant melanoma of the uvea,
XX retinoblastoma, carcinoma of the lacrimal gland, sarcoma of the orbit,
XX brain, spinal cord, vascular system, haemangiosarcoma and Kaposi's
XX sarcoma. The present sequence is human preproheparanase.
XX
XX SQ
XX
XX Sequence 543 AA:
XX
XX Query Match 100.0%; Score 2841; DB 8; Length 543;
XX Best Local Similarity 100.0%; Pred. No. 2.7e-275;
XX Matches 543; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 MLRSKRALPPPLMLLLGLPLSPGALPRPAQADVDLDFPTQPLHLVSPFSVLT 60
XX |||
XX DB 1 MLRSKRALPPPLMLLLGLPLSPGALPRPAQADVDLDFPTQPLHLVSPFSVLT 60
XX |||
XX QY 61 IDANLATDPRFLLILGSPKRLTARGLSPAYLRFGGTGTFLLIDPKKESTPEERSYWG 120
XX |||
XX DB 61 IDANLATDPRFLLILGSPKRLTARGLSPAYLRFGGTGTFLLIDPKKESTPEERSYWG 120
XX |||
XX QY 121 QVNDICKYGSIPPDVEKRLRLEWFOQLLAEHYKRRKNSYSSSDVLYTFANCS 180
XX |||
XX DB 121 QVNDICKYGSIPPDVEKRLRLEWFOQLLAEHYKRRKNSYSSSDVLYTFANCS 180
XX |||
XX QY 181 GLDLIFGLNLRLTADLQNNSSNAQLLDYCSSKGYNISWELGNEPSPFLKKADIFNGS 240
XX |||
XX DB 181 GLDLIFGLNLRLTADLQNNSSNAQLLDYCSSKGYNISWELGNEPSPFLKKADIFNGS 240
XX |||
XX 181 GLDLIFGLNLRLTADLQNNSSNAQLLDYCSSKGYNISWELGNEPSPFLKKADIFNGS 240
XX |||

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Db 241 QUGEDFIQHLKRLKSTFNKAKLYGPDVGQPRRTAKKLSFLKAGGEVIDSVTHHHYLL 300
 QY 301 NGRATREDPLNPDVLDIFISSVQKVFQVVESTPRGKKVWLGETSSAYGGAPLLSDTFA 360
 Db 301 NGRATREDPLNPDVLDIFISSVQKVFQVVESTPRGKKVWLGETSSAYGGAPLLSDTFA 360
 QY 361 AGFWMLDKLGLSARNGIEVVMROVFFGAGNYHLVDENFPLPDYWLSTLFFKLVGTXYLM 420
 Db 361 AGFWMLDKLGLSARNGIEVVMROVFFGAGNYHLVDENFPLPDYWLSTLFFKLVGTXYLM 420
 QY 421 ASVQSKRRKRLRVYLHCTNTDNPRIKEGDLTLVAIINLHVTKYLRPLPYFSNKQVDKXYLL 480
 Db 421 ASVQSKRRKRLRVYLHCTNTDNPRIKEGDLTLVAIINLHVTKYLRPLPYFSNKQVDKXYLL 480
 QY 481 RPLGPHGLLSKSVQJNLGLTKAVDDQTLPLMEKPLRPGSSIGLPAFYSFFVINAKYA 540
 Db 481 RPLGPHGLLSKSVQJNLGLTKAVDDQTLPLMEKPLRPGSSIGLPAFYSFFVINAKYA 540
 QY 541 ACT 543
 Db 541 ACT 543

RESULT 6

ADN05074 strand; protein; 543 AA.

ADN05074;

01-JUL-2004 (first entry)

Antipsoriatic protein sequence #716.

antipsoriatic; gene therapy; psoriasis; diagnosis.

Homo sapiens.

WO2004028479-A2.

08-APR-2004.

25-SEP-2003; 2003WO-US030907.

25-SEP-2002; 2002US-0414006P.

(GETH) GENENTECH INC.

Bodary S, Clark H, Jackman J, Schoenfeld J, Williams PM, Wood WI;

WPI: 2004-305105/28.

N-PSDB; ADN05073.

New PRO nucleic acid or polypeptide, useful for preparing a

pharmaceutical composition for diagnosing or treating psoriasis in a

mammal.

Claim 9; SEQ ID NO 1468; 3069pp; English.

The invention relates to novel polynucleotide and polypeptides for

treating psoriasis or a sequence having at least 80% identity to the

above sequences. The nucleic acid is useful for preparing a composition

for diagnosing or treating psoriasis in a mammal. This sequence

corresponds to one of the polypeptides of the invention.

Sequence 543 AA;

Query Match 100.0%; Score 2841; DB 8; Length 543;

Best Local Similarity 100.0%; Pred. No. 2,7e-275;

Matches 543; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

MLNSKRALPPPLMLLLGLPLSGALPRPAQOVVDLDFPTQEPHLHVSDFLSVT 60

|||||

|||||

Db 1 MLNSKRALPPPLMLLLGLPLSGALPRPAQOVVDLDFPTQEPHLHVSDFLSVT 60
 QY 61 IDANLATDPRFLTLGSPKLTTLARGSPAYLRFGTGTDFLLDPKKESTFEERSYMQS 120
 Db 61 IDANLATDPRFLTLGSPKLTTLARGSPAYLRFGTGTDFLLDPKKESTFEERSYMQS 120
 QY 121 QVNODICKYGSIPDVEBKRLLEMPYQEQLLREHYQKKFKNSTYSSSDVLYTFPANC 180
 Db 121 QVNODICKYGSIPDVEBKRLLEMPYQEQLLREHYQKKFKNSTYSSSDVLYTFPANC 180
 QY 181 GLDLIFGIALLRTRADLOMNSNNAQLLDYSSKGVNISMELGNEPNSFLKKADIFINGS 240
 Db 181 GLDLIFGIALLRTRADLOMNSNNAQLLDYSSKGVNISMELGNEPNSFLKKADIFINGS 240
 QY 241 QUGEDFIQHLKRLKSTFNKAKLYGPDVGQPRRTAKKLSFLKAGGEVIDSVTHHHYLL 300
 Db 241 QUGEDFIQHLKRLKSTFNKAKLYGPDVGQPRRTAKKLSFLKAGGEVIDSVTHHHYLL 300
 QY 301 NGRATREDPLNPDVLDIFISSVQKVFQVVESTPRGKKVWLGETSSAYGGAPLLSDTFA 360
 Db 301 NGRATREDPLNPDVLDIFISSVQKVFQVVESTPRGKKVWLGETSSAYGGAPLLSDTFA 360
 QY 361 AGFWMLDKLGLSARNGIEVVMROVFFGAGNYHLVDENFPLPDYWLSTLFFKLVGTXYLM 420
 Db 361 AGFWMLDKLGLSARNGIEVVMROVFFGAGNYHLVDENFPLPDYWLSTLFFKLVGTXYLM 420
 QY 421 ASVQSKRRKRLRVYLHCTNTDNPRIKEGDLTLVAIINLHVTKYLRPLPYFSNKQVDKXYLL 480
 Db 421 ASVQSKRRKRLRVYLHCTNTDNPRIKEGDLTLVAIINLHVTKYLRPLPYFSNKQVDKXYLL 480
 QY 481 RPLGPHGLLSKSVQJNLGLTKAVDDQTLPLMEKPLRPGSSIGLPAFYSFFVINAKYA 540
 Db 481 RPLGPHGLLSKSVQJNLGLTKAVDDQTLPLMEKPLRPGSSIGLPAFYSFFVINAKYA 540
 QY 541 ACT 543
 Db 541 ACT 543

RESULT 7

ADN04902 strand; protein; 543 AA.

ADN04902;

01-JUL-2004 (first entry)

Antipsoriatic protein sequence #631.

antipsoriatic; gene therapy; psoriasis; diagnosis.

Homo sapiens.

WO2004028479-A2.

08-APR-2004.

25-SEP-2003; 2003WO-US030907.

25-SEP-2002; 2002US-0414006P.

(GETH) GENENTECH INC.

Bodary S, Clark H, Jackman J, Schoenfeld J, Williams PM, Wood WI;

WPI: 2004-305105/28.

N-PSDB; ADN04901.

New PRO nucleic acid or polypeptide, useful for preparing a

pharmaceutical composition for diagnosing or treating psoriasis in a

mammal.

MLNSKRALPPPLMLLLGLPLSGALPRPAQOVVDLDFPTQEPHLHVSDFLSVT 60

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|||||

|||||

[illegible]

	Query Match	Similarity	Score	DB 7	Length	543
	Best Local	Similarity	100.0%	Pred. No.	2.7e-275	
	Matches	543	Conservative	0	Mismatches	0
					Indels	0
					Gaps	0
Qy	1	MLRSKPLPPPLMLLLGPGSPSPGALPPRAQADVDYDLDFPQEPHLTVSBSFLST	60			
Db	1	MLRSKPLPPPLMLLLGPGSPSPGALPPRAQADVDYDLDFPQEPHLTVSBSFLST	60			
Qy	61	IDANLATPREFLLILGSPKRTIARGLSPAYVRFSGTKTDLPDPCKESTFEERSYWS	120			

Db	61	IDANLADTPRFLILIGSGPKRTIARGSLPAYIRFGCTDTDLIPDPKKESTFEERSYWS	120
QY	121	QVNODICKYGSIPDVEEKLRLMEWYOBOLLIREHYOKKFKNSTYSRSSVDVLYTFPANC	180
Db	121	QVNODICKYGSIPDVEEKLRLMEWYOBOLLIREHYOKKFKNSTYSRSSVDVLYTFPANC	180
QY	181	GLDLIFGJNALLRTPADLOWNSSNALLDYCSKRYN1SWEIGNPNISGLKKAIDIFINGS	240
Db	181	GLDLIFGJNALLRTPADLOWNSSNALLDYCSKRYN1SWEIGNPNISGLKKAIDIFINGS	240
QY	241	QLGEDFIOHLHLRKRSTFKNAKLYPBDVGOPRRKPAKMLKSPFLKAGGEVIDSVTWHYYL	300
Db	241	QLGEDFIOHLHLRKRSTFKNAKLYPBDVGOPRRKPAKMLKSPFLKAGGEVIDSVTWHYYL	300
QY	301	NGRTATREDPLNPVDVLDFISSQVKVFOVBESTRPGKKVWLGETSSAYGGAPLLSDTFA	360
Db	301	NGRTATREDPLNPVDVLDFISSQVKVFOVBESTRPGKKVWLGETSSAYGGAPLLSDTFA	360
QY	361	AGFWMLDLKGLSARMGIEVVMRQVFFGAGNHLVBENPDLDPYMLSLFLKLVGRKULM	420
Db	361	AGFWMLDLKGLSARMGIEVVMRQVFFGAGNHLVBENPDLDPYMLSLFLKLVGRKULM	420
QY	421	ASVQGSKRKRLRVYLHCTNTDNPRLKEGBDLTYALNLNHWTKYLRLPYFPSKNQVDKYL	480
Db	421	ASVQGSKRKRLRVYLHCTNTDNPRLKEGBDLTYALNLNHWTKYLRLPYFPSKNQVDKYL	480
QY	481	RPLGPHGLSSKSVQJNLGLTKXVDDQTLPLMEKEPLRPOSSLGDLPAFSYSPFVIRNAKYA	540
Db	481	RPLGPHGLSSKSVQJNLGLTKXVDDQTLPLMEKEPLRPOSSLGDLPAFSYSPFVIRNAKYA	540
QY	541	ACI 543	
Db	541	ACI 543	

```

RESULT 4
ADK52086
ID ADK52086 standard; protein, 543 AA.
XX
AC ADK52086;
XX
DT 20-MAY-2004 (first entry)
XX
DE Human atopic dermatitis/psoriasis-associated protein #1.
XX
KW Human; atopic dermatitis; psoriasis; dermatological; anti-inflammatory
XX antipsoriatic; rash.
XX
OS Homo sapiens.
XX
PN WO2004016785-A1.
XX
PD 26-FEB-2004.
XX
PF 06-AUG-2003; 2003WO-JP009999.
XX
PR 06-AUG-2002; 2002JP-00229319.
XX
PR 14-MAY-2003; 2003JP-00136544.
XX
PA (GENO-) GENOX RES INC.
XX (UYJU-) UNIV JUJUNENDO.
XX
PI Itoh M, Ogawa K, Shinagawa A, Sudo H, Ogawa H, Ra C;
XX Mitsuishi K;
XX
XX WPI; 2004-214514/20.
XX
DR N-PSDB; ADK51968.
XX
PT Detecting atopic dermatitis or psoriasis comprises assaying levels of
XX expression of an indicator gene at a rash site and non-rash site of a
XX person with atopic dermatitis or psoriasis.
XX

```

CC above can be diagnosed using specific antibodies, and also using primers
CC and probes specific for the heparanase polynucleotides. Other uses of the
CC heparanases include sequencing sulfated molecules such as HSPG. The
CC present sequence represents a human heparanase

XX Sequence 543 AA;

Query Match 100.0%; Score 2841; DB 2; Length 543;
Best Local Similarity 100.0%; Pred. No. 2.7e-275; Indels 0; Gaps 0;
Matches 543; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

OY 1 MLRSKPALPPMLLLGLPLSPGALPRPAQADVVDLDFTEQEPHLVSPSLSYT 60
DB 1 MLRSKPALPPMLLLGLPLSPGALPRPAQADVVDLDFTEQEPHLVSPSLSYT 60
OY 61 IDANLATDPRFLILGSPKRTLARGSPAYLRFGCTKTDPLIPDKKSTFEERSYWS 120
DB 61 IDANLATDPRFLILGSPKRTLARGSPAYLRFGCTKTDPLIPDKKSTFEERSYWS 120
OY 121 QVNODICKYGSIPDVEEKLRLMPYQEQQLLREHYOKKFNSTYSRSSVDVLYTFPANC 180
DB 121 QVNODICKYGSIPDVEEKLRLMPYQEQQLLREHYOKKFNSTYSRSSVDVLYTFPANC 180
OY 121 QVNODICKYGSIPDVEEKLRLMPYQEQQLLREHYOKKFNSTYSRSSVDVLYTFPANC 180
DB 121 QVNODICKYGSIPDVEEKLRLMPYQEQQLLREHYOKKFNSTYSRSSVDVLYTFPANC 180
OY 181 GIDLIFGLNALIRTDALQWSSNAQLLDYCSSKGYNISWELGNEBNSFLKKADIFINGS 240
DB 181 GIDLIFGLNALIRTDALQWSSNAQLLDYCSSKGYNISWELGNEBNSFLKKADIFINGS 240
OY 241 QUGGEPIQHLKLRSTFNKATLYGPDVGQPRKTKAKMLKSLFKAGGEVIDSTVTHHHYLL 300
DB 241 QUGGEPIQHLKLRSTFNKATLYGPDVGQPRKTKAKMLKSLFKAGGEVIDSTVTHHHYLL 300
OY 301 NGRTATREDPLNPVDLDFISSVQKVFQVVESTPGKATWLGSTSSAYGGAPLLSDTPA 360
DB 301 NGRTATREDPLNPVDLDFISSVQKVFQVVESTPGKATWLGSTSSAYGGAPLLSDTPA 360
OY 361 AGFMWLDKLGISARWGIEVVMRQVFFGAGNYHLVDENFDPLPDYWLSTLLFKKLVTGKVL 420
DB 361 AGFMWLDKLGISARWGIEVVMRQVFFGAGNYHLVDENFDPLPDYWLSTLLFKKLVTGKVL 420
OY 421 ASVOGSKRRKRLRVYLHCTNDNPRYKEDDLTYAINLHVNTKYLRPPFSKKQVDKYL 480
DB 421 ASVOGSKRRKRLRVYLHCTNDNPRYKEDDLTYAINLHVNTKYLRPPFSKKQVDKYL 480
OY 481 RPLGPHGLSKSVQNLGLTLKKVDDQTLPLMEKPLRPGSSLGLPAPFSYFVIRNAKYA 540
DB 481 RPLGPHGLSKSVQNLGLTLKKVDDQTLPLMEKPLRPGSSLGLPAPFSYFVIRNAKYA 540
OY 541 ACI 543
DB 541 ACI 543

```

RESULT 2

AAB86206
ID AAB86206 standard; protein; 543 AA.

AC AAB86206;

XX 24-AUG-2001 (first entry)

XX Human heparanase inhibitor protein.

XX Heparanase; inhibitor; cardiac insufficiency; cardiatic; nephrotropic;

XX hepatocytic; veterinary medicine; congestive heart failure; dyspnoea;

XX primary cardiomyopathy; peripheral odema; pulmonary congestion;

XX hepatic congestion; hydrothorax; ascite; nocturia; human.

OS Homo sapiens.

XX DE19955803-A1.

XX 23-MAY-2001.

PF 19-NOV-1999; 99DE-01055803.
XX
PR 19-NOV-1999; 99DE-01055803.
XX

PA (KNOL) KNOL AG.

PI Herr D, Hahn A, Laux V;

XX WPI: 2001-368371/39.

DR N-PSDB; AAH20940.

PT Treatment or prevention of cardiac insufficiency and related conditions,
PT e.g. pulmonary congestion and dyspnoea, comprises administration of
PT heparanase inhibitor.

PS Disclosure; Page 11-13; 16pp; German.

CC This invention describes a novel heparanase inhibitor which can be used
CC for the treatment or prevention of cardiac insufficiency and associated
CC indications, symptoms and/or malfunctions. The heparanase inhibitor of
CC the invention has cardiatic, nephrotropic and hepatotropic activity. The
CC products of the invention can be used in human and veterinary medicine,
CC for the treatment or prevention of congestive heart failure e.g. primary
CC cardiomyopathy. Associated conditions treated or prevented with the
CC inhibitor are especially peripheral odemas, pulmonary and hepatic
CC congestion, dyspnoea, hydrothorax and ascites. Renal problems, e.g.
CC nocturia can also be treated. This sequence represents the human
CC heparanase protein described in the method of the invention

XX Sequence 543 AA;

Query Match 100.0%; Score 2841; DB 4; Length 543;
Best Local Similarity 100.0%; Pred. No. 2.7e-275; Indels 0; Gaps 0;
Matches 543; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

OY 1 MLRSKPALPPMLLLGLPLSPGALPRPAQADVVDLDFTEQEPHLVSPSLSYT 60
DB 1 MLRSKPALPPMLLLGLPLSPGALPRPAQADVVDLDFTEQEPHLVSPSLSYT 60
OY 61 IDANLATDPRFLILGSPKRTLARGSPAYLRFGCTKTDPLIPDKKSTFEERSYWS 120
DB 61 IDANLATDPRFLILGSPKRTLARGSPAYLRFGCTKTDPLIPDKKSTFEERSYWS 120
OY 121 QVNODICKYGSIPDVEEKLRLMPYQEQQLLREHYOKKFNSTYSRSSVDVLYTFPANC 180
DB 121 QVNODICKYGSIPDVEEKLRLMPYQEQQLLREHYOKKFNSTYSRSSVDVLYTFPANC 180
OY 121 QVNODICKYGSIPDVEEKLRLMPYQEQQLLREHYOKKFNSTYSRSSVDVLYTFPANC 180
DB 121 QVNODICKYGSIPDVEEKLRLMPYQEQQLLREHYOKKFNSTYSRSSVDVLYTFPANC 180
OY 181 GIDLIFGLNALIRTDALQWSSNAQLLDYCSSKGYNISWELGNEBNSFLKKADIFINGS 240
DB 181 GIDLIFGLNALIRTDALQWSSNAQLLDYCSSKGYNISWELGNEBNSFLKKADIFINGS 240
OY 241 QUGGEPIQHLKLRSTFNKATLYGPDVGQPRKTKAKMLKSLFKAGGEVIDSTVTHHHYLL 300
DB 241 QUGGEPIQHLKLRSTFNKATLYGPDVGQPRKTKAKMLKSLFKAGGEVIDSTVTHHHYLL 300
OY 301 NGRTATREDPLNPVDLDFISSVQKVFQVVESTPGKATWLGSTSSAYGGAPLLSDTPA 360
DB 301 NGRTATREDPLNPVDLDFISSVQKVFQVVESTPGKATWLGSTSSAYGGAPLLSDTPA 360
OY 361 AGFMWLDKLGISARWGIEVVMRQVFFGAGNYHLVDENFDPLPDYWLSTLLFKKLVTGKVL 420
DB 361 AGFMWLDKLGISARWGIEVVMRQVFFGAGNYHLVDENFDPLPDYWLSTLLFKKLVTGKVL 420
OY 421 ASVOGSKRRKRLRVYLHCTNDNPRYKEDDLTYAINLHVNTKYLRPPFSKKQVDKYL 480
DB 421 ASVOGSKRRKRLRVYLHCTNDNPRYKEDDLTYAINLHVNTKYLRPPFSKKQVDKYL 480
OY 481 RPLGPHGLSKSVQNLGLTLKKVDDQTLPLMEKPLRPGSSLGLPAPFSYFVIRNAKYA 540
DB 481 RPLGPHGLSKSVQNLGLTLKKVDDQTLPLMEKPLRPGSSLGLPAPFSYFVIRNAKYA 540
OY 541 ACI 543
DB 541 ACI 543

```

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OM protein - protein search, using sw model

Run on: March 23, 2005, 11:09:57 ; Search time 113.5 Seconds
(without alignments)
1850.316 Million cell updates/sec

Title: SEQ2B
Perfect score: 2841
Sequence: 1 MLIRSKPALPPIMLLIGP.....LPAFSYSPFVIRNAKVAACI 543

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues
Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_16Dec04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2841	100.0	543	2	AAV17082 Human hep
2	2841	100.0	543	4	AAB86206 Human hep
3	2841	100.0	543	7	ADDI8950 Human dis
4	2841	100.0	543	8	AdK52086 Human atc
5	2841	100.0	543	8	ADMA48759 Human hpa
6	2841	100.0	543	8	ADN05074 Antipscot
7	2841	100.0	543	8	ADN04902 Antipscot
8	2841	100.0	543	8	ADQ80372 Heparanas
9	2841	100.0	543	8	ADR88210 Human pre
10	2841	100.0	543	8	ADP25079 PRO polyp
11	2841	100.0	568	2	AAV30124 A human p
12	2838	99.9	543	2	AAV02345 A human h
13	2838	99.9	543	3	AAV57590 Human hep
14	2838	99.9	543	3	AAB08849 Amino aci
15	2838	99.9	543	3	AAV52990 Human hep
16	2838	99.9	543	4	AAV97635 Human hep
17	2838	99.9	543	5	ABR07813 Human hep
18	2838	99.9	543	7	ADG88800 Human hpa
19	2838	99.9	543	8	ADL16379 Human hep
20	2838	99.9	543	8	ADMA48716 Human hpa
21	2838	99.9	592	2	AAV02346 A human h
22	2838	99.9	592	3	AAB08850 Amino aci
23	2838	99.9	592	7	ADG88804 Human SK-
24	2838	99.9	592	8	ADL16383 Human hep
25	2838	99.9	592	8	ADMA48720 Human SK-

26	2835	99.8	543	8	AD063831 Human hep
27	2835	99.8	543	8	AD063823 Human hep
28	2835	99.8	543	8	AD063832 Human hep
29	2835	99.8	543	8	AD063822 Human hep
30	2829	99.6	543	4	AAB88361 Human mem
31	2829	99.6	543	8	AD063824 Human hep
32	2820	99.3	545	6	ABP56822 Human hep
33	2820	99.3	545	7	ADL16012 Human G-c
34	2820	99.3	545	8	ADL93951 Human G-c
35	2767	97.4	530	2	AAV34173 Human pre
36	2740	96.4	532	2	AAV17083 Seg ID No
37	2676.5	94.2	527	5	ABR07815 Chicken b
38	2676.5	94.2	527	7	ABR02018 Chimeric
39	2670.5	94.0	527	8	AD063825 Chimeric
40	2670.5	94.0	527	8	AD063826 Chimeric
41	2664.5	93.8	527	8	AD063827 Chimeric
42	2149	75.6	535	3	AAB08851 A murine
43	2149	75.6	535	5	ABR07811 Mouse hep
44	2149	75.6	535	7	ADG88834 Mouse hpa
45	2149	75.6	535	8	ADL16413 Mouse

ALIGNMENTS

AAV17082	AAV17082 standard; protein; 543 AA.
AC	AAV17082;
DT	21-JUL-1999 (first entry)
DE	Human heparanase enzyme.
XX	Heparanase; endoglucuronidase; heparan sulfate proteoglycan; enzyme; metacastis; angiogenesis; wound healing; angioplasty-induced restenosis; arteriosclerosis; atherosclerosis; inflammation; tissue development; human; HSPG.
XX	Homo sapiens.
OS	
XX	
PN	WO921975-A1.
XX	06-MAY-1999.
PF	28-OCT-1998; 98WO-AU000898.
XX	
PR	28-OCT-1997; 97AU-0000062.
XX	09-DEC-1997; 97AU-00000812.
PA	(AUSU) UNIV AUSTRALIAN NAT.
XX	
PI	Freeman CG, Hulett MD, Parish CR, Hamdorf BJ,
XX	WPI; 1999-312956/26.
DR	N-PSDB; AAX37259.
XX	
PT	Polynucleotides encoding mammalian endoglucuronidases, especially heparanases, useful to promote wound healing.
XX	
PS	Claim 6; Page 69-73; 112pp; English.
XX	
CC	The invention relates to nucleic acid sequences that encode heparanase enzymes having endoglucuronidase activity. Recombinant heparanases are capable of removing the HS side chain from heparan sulfate proteoglycan (HSPG). Sulfated oligosaccharides, sulphonates or HSPG can be used to inhibit heparanase, this is useful for treatment of a physiological or medical condition associated with elevated heparanase activity, such as metastasis, angiogenesis, wound healing, angioplasty-induced restenosis, arteriosclerosis, atherosclerosis and inflammation. The human, murine and rat heparanases can be used to enhance wound healing, especially associated with tissue development and repair. The conditions mentioned

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```
QY 27 GALPPPAQADVVDLDFTEQEPHLVSPSFLSVTTIDA---NLATDPRF-LIILGSPKLT 82
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 238 GKKEPFVBEDEETMKMAETLDTYTEETLNIQKARENNDCSRPKMWTLPK--- 294
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 83 IARGSPAYLRFGGTQDTFLIPDPKKESTFEERSYQSOVNODICKYGSIPPDVEEKLRL 142
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 295 -----GWTGPKFV-----DGVNPGSFPRAHQVPLAVDRYHTENDQLE---- 332
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 143 EW--PYQEQLLIREHYQ--KKERNSTYSSSVDLVTFPANCGLDLIFGLNALLRTADIQ 198
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 333 EWLKSKYPEELFEDENYRLIPLEBELTPKGNKRMAMNLMAN--GGL-----LRLRLPPDR 386
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 199 WNSSNAQQLLDYCSSGNYNISMELGNEPNSFLKKADIFPNSQGLGDFIQHLKLR---- 254
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 387 -----DYA-----VDVPTPGSTVQDMTELKRYADVVK 415
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 255 -KSTFNNAKLYGPD-----VGQPRRKTKAKMLK--SFLKAGEVIDSVTWH-- 297
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 416 LNEEDTRNFRIFGPDETRMSRLMAVFEGRKQWLSEIKENDEFLSMDGRIVDSMLSEHLG 475
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 298 -----YINGRTATREDFLNPDVLDIFISSVQKVFQVES--TRPKKVMIGETS 345
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 476 EGMLEGYLLTGRHG-----FPASYEAPLRIVDSMITQHGK--WLKVTS 516
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
```

RESULT 15

```
At1489
probable peptidoglycan bound protein (LPTXG motif) lin0457 [imported] - Listeria innocua
C:Species: Listeria innocua
C:Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004
C:Accession: At1489
R:Glaer, P.; Frangoul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloeker,
.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Feihl, H.
D.; Jones, L.M.; Karst, U.
Science 294, 849-852, 2001
A:Authors: Krefc, J.; Kuhn, M.; Kunst, F.; Kurapkac, G.; Madueno, E.; Maltournam, A.; Ma
ok, C.; Schluter, T.; Simoes, N.; Tlerez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland,
A.; Title: Comparative genomics of Listeria species
A:Reference number: AB1077; NCID:21537279; PMID:11679669
A:Accession: At1489
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-2013 <GLA>
A:Cross-references: UNIPROT:Q92EK2; GB:AL592022; PDB:1CAG5689.1; PDB:1G1412898; GSPDB:G
A:Experimental source: strain Clp11262
C:Genetics:
A:Gene: lin0457
```

Query Match 3.7%; Score 104; DB 2; Length 2013;
Best Local Similarity 20.6%; Pred. No. 62;
Matches 95; Conservative 64; Mismatches 161; Indels 142; Gaps 21;

```
QY 5 SKPALPPMLLLGLPLSPGALPPPAQADVVDL-----FFT 45
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 256 AKRGVVMNLKATL---SGENSAGATYTPAKKTTVNLBEENSNLDYSPITAGDNWAFSW 312
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 46 QEPHLVSPSFLSV---TIDANLATDPRFLLILGSPKLTARG-----LSPAYLR 93
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 313 KEIAPFLKPGGYTIQWPEIQKSEKNSFKNL---KLEFLKENGDDIISVNTADPYVIR 368
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 94 FG-----GTKTDPLIFDPKKESTFEERSYQSOVNODICKYGSIPPDVEEKLRL 143
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 369 FGEPPYQSJSTVNGKANVLVNDDEKO-----VVEIGPINANITYQRIQVS 412
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 144 WP-----YQEQLLIREHYQKKFNSTYSSSVDLVTFPANCGLDL 184
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 413 MAKIPADAVKGTGYGVVVDLIVTSIKIKTEVTDATSIAVDSKVSKTISRGDV 472
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 185 IFGLNALIRTADLOMN-----SSNA-----QLLDYCSKGYNI--SWELGNEPNSFLKAD 234
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 473 -----LWGMFPRISAAAPGVNDLEIVAPIPKGIKVLSTYIPNNNSMASMKKLE 520
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
```

```
QY 235 IFING-----SQLGEDFIQLHKLRL-----KSTFNNAKLYGPDVGQPRRKAKMLKS 281
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 521 YQNGKQWVSMAPQTSQSSGMDFSKIDQSVNRIEKLTLSRDLINDKMDPPYTHGTRMQWT 580
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 282 FLKAGGEVY---DSYTMHHYILNGRTATREDFLNPDVLDIFISSVQKVFQVEST--RPGK 337
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 581 GYKAGESFTLOPESIT---YTDSDKTS-----KALDTNASSYEKKVQVEKSTSPAK 629
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 338 ---KVMIGETSAVYGGAPLLSDTFAAGFMMLDKLGLSARWG 376
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 630 INGDFVLSSTAGIYQKG--FESTIFNG---DKIAQSVRLG 665
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
```

Search completed: March 23, 2005, 11:31:41
Job time : 29 secs

RESULT 12

S00652

phosphoribosylamine-glycine ligase (EC 6.3.4.13) - fission yeast (*Schizosaccharomyces pombe*)
 NAlternate names: AIRase, aminimidazole ribotide synthetase, GARSae, glycylamide rib N-contains: phosphoribosylamine-glycine ligase (EC 6.3.4.13); phosphoribosylformylglycin C;Species: *Schizosaccharomyces pombe*
 C;Date: 07-Sep-1990 #sequence revision 28-Oct-1994 #text_change 09-Jul-2004

A;Accession: S00652; T40496; T40422

R;McKenzie, R.; Schuchert, P.; Kibbey, B.

Curr. Genet. 12, 591-597, 1987

A;Title: Sequence of the bifunctional ade1 gene in the purine biosynthetic pathway of th

A;Reference number: S00652; M01D:89003164; PMID:3502942

A;Accession: S00652

A;Molecule type: DNA

A;Residues: 1-788 <MCK>

A;Cross-references: UNIPROT:P20772; EMBL:X06601; NID:g4903; P1DN:CAA29820.1; PID:g4904

R;Wood, V.; Rajandream, M.A.; Barrell, B.G.; Lauber, J.; Hiltbert, H.; Duesterhoeft, A.

submitted to the EMBL Data Library, February 1998

A;Reference number: Z21910

A;Accession: T40496

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 1-788 <MOO>

A;Cross-references: EMBL:AL021730; P1DN:CAA16823.1; GSPDB:GN00067; SPDB:SPBC4C3.02c

A;Experimental source: strain 972h; cosmid c4C3

R;Seeger, K.; Harris, D.; Wood, V.; Rajandream, M.A.; Barrell, B.G.

submitted to the EMBL Data Library, March 1999

A;Reference number: Z21928

A;Accession: T40422

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 604-788 <SEE>

A;Cross-references: EMBL:AL035655; P1DN:CA838600.1; GSPDB:GN00067; SPDB:SPBC405.01

A;Experimental source: strain 972h; cosmid c405

A;Accession: S00652

A;Molecule type: DNA

A;Residues: 1-788 <MOO>

A;Cross-references: EMBL:AL021730; P1DN:CAA16823.1; GSPDB:GN00067; SPDB:SPBC4C3.02c

A;Experimental source: strain 972h; cosmid c4C3

R;Seeger, K.; Harris, D.; Wood, V.; Rajandream, M.A.; Barrell, B.G.

submitted to the EMBL Data Library, March 1999

A;Reference number: Z21928

A;Accession: T40422

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 604-788 <SEE>

A;Cross-references: EMBL:AL035655; P1DN:CA838600.1; GSPDB:GN00067; SPDB:SPBC405.01

A;Experimental source: strain 972h; cosmid c405

A;Accession: S00652

A;Molecule type: DNA

A;Residues: 1-788 <MCK>

A;Cross-references: UNIPROT:P20772; EMBL:X06601; NID:g4903; P1DN:CAA29820.1; PID:g4904

R;Wood, V.; Rajandream, M.A.; Barrell, B.G.; Lauber, J.; Hiltbert, H.; Duesterhoeft, A.

submitted to the EMBL Data Library, February 1998

A;Reference number: Z21910

A;Accession: T40496

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 1-788 <MOO>

A;Cross-references: EMBL:AL021730; P1DN:CAA16823.1; GSPDB:GN00067; SPDB:SPBC4C3.02c

C;Accession: F70411

R;Decker, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.E.; Oye

V.

Nature 392, 353-358, 1998

A;Title: The complete genome of the hyperthermophilic bacterium *Aquifex aeolicus*.

A;Reference number: A70300; M01D:98196666; PMID:9537320

A;Accession: F70411

A;Status: preliminary; nucleic acid sequence not shown; translation not shown

A;Molecule type: DNA

A;Residues: 1-432 <AQF>

A;Cross-references: UNIPROT:O67321; GB:AE000733; NID:g2983720; P1DN:AA07286.1; PID:g2983

A;Experimental source: strain VFS

C;Genetics:

A;Gene: purA

C;Superfamily: adenylosuccinate synthase

Query Match 3.7%; Score 104; DB 2; Length 432;

Best Local Similarity 23.9%; Pred. No. 6.2;

Matches 96; Conservative 39; Mismatches 128; Indels 138; Gaps 22;

15 LLLGLGPGSPGALPRPAQDVVDLD-----FTQBPMLVSPS 55

51 ILHLPTGLHGHVGVINQGM-VVDLEVLHKEVKNLEKGIYKRLTSDRAHLMPY 109

56 FLVITDANLADPPFLILGSPK--LRTIANGLSPAY-REGTKTDFLIDPKKESTF 112

110 H-----KLDLFLFKKKIGICTTLAGIGAVFKG--RKGIKISDLKDEKRF 154

113 EERSTWQOVNODICKYSGISPPDVEEK-----LRLEMPYQOLLRHRYQKKFNSTY 165

155 ----YTLLEDNLDLPVK-----NICEKVCERFDLDINOIYEOUL-----RYEEFKEVN- 199

166 SRSVDVLTYPANCSGLDIFGLNLLTRADL-----QWNSNAQQLLDYCSSKGVNISM 221

200 ----VDLRFPTQKQSVLPFGAQGTLDVDGTYPTVSSNSAL-----GLSNG 246

222 LGNBNPSFLKADIFING-----SQI-GEF1QLHLKSTFKNAKYG 265

247 TGMPPRYF--SDAFLVGVAKAYTRVGGPPPTLKGEGEKLRRL-----CGERG 295

266 PDVGQPR--KTAKMLKFLAAGEVIDSVTHHYLNGRATREDFLNP----- 313

296 STYGRPRRCGMLDLVALKTAQVNG-----LDGFIYTKDVLDTDEVKCV 343

314 ----DVLDIFISSVQKQVQV--VESTPRGKVMLGESSA 347

344 YELDEVIDYFPASYSSELIRKPVYKTLKG---WKKSTXGA 381

RESULT 14

D97065

transketolase [imported] - Clostridium acetobutylicum

C;Species: Clostridium acetobutylicum

C;Date: 14-Sep-2001 #sequence revision 14-Sep-2001 #text_change 09-Jul-2004

R;Colling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee,

J.; Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.

J. Bacteriol. 183, 4823-4838, 2001

A;Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Clo

A;Reference number: A96900; M01D:21359325; PMID:21359325

A;Accession: D97065

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-796 <KUR>

A;Cross-references: UNIPROT:Q97JF3; GB:AE001437; P1DN:AAK79311.1; PID:g15024275; GSPDB:G

A;Experimental source: Clostridium acetobutylicum ATCC824

C;Genetics:

A;Gene: CAC1343

C;Superfamily: phosphoketolase

Query Match 3.7%; Score 104; DB 2; Length 796;

Best Local Similarity 21.6%; Pred. No. 15;

Matches 77; Conservative 51; Mismatches 114; Indels 114; Gaps 18;

```

QY          416 TKVLMAV 423
      | | :
Db          401 LKSLHMQ 408

RESULT 11
E91031
Probable outer membrane protein ECS3221 [imported] - Escherichia coli (strain O157:H7, su
C/Species: Escherichia coli
C/Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #ext_change 09-Jul-2004
C/Accession: E91031
R/Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.;
gsawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
DNA Res. 8, 11-22, 2001
A/Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and genom
A/Reference number: A99625; MUID:21156231; PMID:11258796
A/Accession: E91031
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-879 <HAV>
A/Cross-references: UNIPROT:Q8XCP4; GB:BA000007; PIDD:BAH36644.1; PIDD:G13362691; GSPDB:GN
A/Experimental source: strain O157:H7, substrain RIMD 0509952
C/Genetics:
A/Gene: ECS3221

Query Match          3.7%; Score 105.5; DB 2; Length 879;
Best Local Similarity 19.9%; Pred. No. 14;

```

[illegible][illegible]

QY 256 -----STFKN--AKLYGPDVGQPRRTAKMLKSFLLKAGGEV-----IDSV 293
 DB 341 DYKDFHIGVITKYLNSGFKNKNNSTLMTSSKTQDRKSHNMSSILDDGNKTMGVSPIDE- 399
 QY 294 TWHHYYLNG-----RTATREDFLNPVDLDTISSVQKVPQVSESTR--PGKK 338
 DB 400 -YSHFIDNDEPLMRDKVKVPKTYNTEGTPPDASAIFFDS--HKIYALISLLRYLPEKR 454

RESULT 7

hypothetical protein MJ0670 - Methanococcus jannaschii

C:Species: Methanococcus jannaschii
 C:Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004

C:Accession: F64383
 R:Bult, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blake, R.; Reich, C.I.; Overbeek, R.; Kirkness, E.F.; Weinstock, K.G.; Merrick, J.M.; Glodek, A.; Keon, J.D.; Sadow, P.W.; Hanna, M.C.; Cotton, M.D.; Roberts, K.M.; Hurst, M.A.
 Science 273, 1058-1073, 1996
 A:Authors: Kaine, B.P.; Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; Woese, C.
 A:Title: Complete genome sequence of the methanogenic archaeon, Methanococcus jannaschii
 A:Reference number: A64300; MUID:96337999; PMID:8688087
 A:Accession: F64383
 A:Status: preliminary; nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-356 <BUL>
 A:Cross-references: UNIPROT:Q58084; GB:U67514; GB:L77117; NID:92826304; PIDN:AA98664.1;
 C:Genetics:
 A:Map position: REV596956-595886
 A:Start codon: GTG

Query Match 3.9%; Score 110.5; DB 2; Length 356;
 Best Local Similarity 21.0%; Pred. No. 1.5; Mismatches 155; Indels 105; Gaps 15;
 Matches 82; Conservative 49;

QY 126 ICKY-----GSIPDVEKRLLEMPYQEQLLREHYQKKFKNSTYSSVD----- 171
 DB 14 IRRKMYGVGNKBEKDKERLKE-----LKEEHVLETEDEGTYYLKADEBEEMHSHV 66
 QY 172 -----VLYTFANCSGDLIFGLNALIRTDLDQNNNAQLLDYCSKGYNISMEIGNP 226
 DB 67 GALKKAIYFAKPS-----KIDL-----SNPR-VLDLCSGMGYNAIAALHYNK 109
 QY 227 NSFLLKADIF-----INGSQLGDFIQLHKLKSTFKNAKLYGPDV 268
 DB 110 NAEIDMVEICEEVLPTLFLDPYKHEIKDKVRFYFLANKIGIEKSYDINLY---V 166
 QY 269 GQPRRTAKMLKSFLLKAGGEVIDSVTHHHYYLNGRTAT--REDFLNPVDLDTISSVQKV 326
 DB 167 GDAKRFIIKSDKKY-----NVVEHDAFSPKRDPTLYYDFL-----KEI 205
 QY 327 PQVVESTRGKVKWLGESAYGGAPLSDTFAGFPMLDLGLSARMGIEVVMQVFP 386
 DB 206 YKRMEN--GVLI-----SYSSALPFRSALVDCFFVISEKSVKRGKITLAYNPNF 256
 QY 387 GAGNYHVLVDENPD-----PLPDYWLILFLKLVGTGYLMAVSGSKRKLRYVLAHTN 439
 DB 257 KENRINEVDERVIALSVIALPYRDETLSTKDKIIDREBRKLEKLIKIGYLTSTQ 316
 QY 440 TQNPYKEDDLTYA--INLHNTKYLRLPY 468
 DB 317 IKGNIPPEILKIQKEDLNSSEIKKGRKF 347

RESULT 8

beta-fructofuranosidase (EC 3.2.1.26) - fava bean

C:Species: Vicia faba (fava bean)
 C:Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004

C:Accession: T12094
 R:Weber, H.; Borisjuk, L.; Heim, U.; Buchner, P.; Wobus, U.
 Plant Cell 7, 1835-1846, 1995

A:Title: Seed coat-associated invertases of fava bean control both unloading and storage

A:Reference number: Z17416; MUID:96093423; PMID:8535137

A:Accession: T12094
 A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-575 <WEB>
 A:Cross-references: UNIPROT:Q43855; EMBL:Z35162; NID:9861154; PIDN:CAA84526.1; PID:98611;
 A:Experimental source: cv. Fibo, seed coat

C:Genetics:
 A:Gene: CWINV1

C:Superfamily: beta-fructofuranosidase
 C:Keywords: cell wall; glycoprotein; glycosidase; hydrolase

Query Match 3.8%; Score 107.5; DB 2; Length 575;
 Best Local Similarity 21.1%; Pred. No. 5.2;
 Matches 71; Conservative 49; Mismatches 107; Indels 109; Gaps 19;

QY 46 QEPHLVS-----PSFLSVITDANLATDPFLLILSPKRLTLARGIS-----P 89
 DB 228 KPHISAKRTGMECPDFPVPVLEKRGD--LSMMGNVHVKNSLDITREYTYTG 285
 QY 90 AYLR-----FGTKTDF-----LIFDPKKESTFEERSYV-----QSQVNG 124
 DB 286 TYLQNDQKTIPTKTEDEGGLRVDYGNFYASKSFDPYK---NRIITGMANESDTKE 341
 QY 125 DICKYG-----SIPDV-----EKKRLLEMPYQEQLLR-----EHYQKKFKNSTYSSSV 170
 DB 342 DQVKGGMAGIQAIPTVWLDSSRQLR-QWVPELNLRLRGKVEMKNRLKXGGY----L 396
 QY 171 DVLTFPANCSDGLIFGLNALIRTDLDQNNNAQLLDYCSKGYNISMEIGNEPNTL 230
 DB 397 EVKGITASQADVEVTFSSLDKAEAFDPNMENAE--DLCKQKSKYGVGV--PFGLL 451
 QY 231 KKADIFINSQGEPIQ-----HKLL-----RKSTPKNAKLYGP-----DV 268
 DB 452 TLA-----SKLEETVTSVFRVFKAAKHKILMSDAKSSLSNRLYPSFAGFVNVDL 505
 QY 269 GQPRRTAKMLKSFLLKAGGEVIDSVTHHHYYLNGRT 304
 DB 506 GNNKKLSLRSI-----IDHSVSEFVGKRT 531

RESULT 9

microtubule-associated protein sm4 - fission yeast (Schizosaccharomyces pombe)

C:Species: Schizosaccharomyces pombe
 C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004

C:Accession: T38446; T00012
 R:McDougall, R.; Wood, V.; Barrell, B.G.; Rajandream, M.A.
 submitted to the EMBL Data Library, December 1997

A:Reference number: Z21793
 A:Accession: T38446

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-670 <MCD>
 A:Cross-references: UNIPROT:Q42667; EMBL:AL009227; PIDN:CAA15832.1; GSPDB:GN00066; SPDB:6

A:Experimental source: strain 97zh; cosmid c27D7

R:Yamashita, A.; Watanabe, Y.; Yamamoto, M.
 Genes to Cells 2, 155-166, 1997

A:Title: Microtubule-associated coiled-coil protein Sm4 is involved in the meiotic deve]

A:Reference number: Z14042; MUID:97311255; PMID:9167972

A:Accession: T00012
 A:Status: translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-670 <YAM>
 A:Cross-references: EMBL:AB000269; NID:93341860; PIDN:BAJ31857.1; PID:93341861

C:Genetics:
 A:Gene: sm4; SPAC27D7.13c
 A:Map position: 1

Query Match 3.7%; Score 106; DB 2; Length 670;
 Best Local Similarity 21.4%; Pred. No. 8.5; Mismatches 149; Indels 86; Gaps 15;
 Matches 80; Conservative 58;


```
QY 411 KLVGTGYLMASVQSKRR-----KLRYLHCTNTDNPYKEDLTLYAINHNT 461
DB 337 KRLIPKYLAVAVAGLQKRPGRVIRDLKRIYACHTNHHNNYRGSTLTFLINLHR 396
QY 462 KYLRLLPYPPSKNOVDKYLRIPGLGSLKSVQVNLGLTKMVDQTLPLMEKPLRPGSS 521
DB 397 KIKIKAGTLRDLVHGYLLQPYGQEGLSKSKSVQLNGQPLVMVDGTLPELKEPRLRAGR 456
QY 522 LGLPAFSYFFYIRNAKVAAC 542
DB 457 LVIPPTMGFFVKKVNNALAC 477

RESULT 2
T45608
Hypothetical protein F13G24.30 - Arabidopsis thaliana
C/Species: Arabidopsis thaliana (mouse-ear cress)
C/Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 09-Jul-2004
C/Accession: T45608
R/Bevan, M.; Van Der Schueren, J.; Chung, Y.J.; Voel, M.; Robben, J.; Volckaert, G.; Be
submitted to the Protein Sequence Database, December 1999
A/Reference number: Z23009
A/Accession: T45608
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-521 <BEV>
A/Cross-references: UNIPROT:Q9SDA1; EMBL:AL133421
A/Experimental source: cultivar Columbia; BAC clone F13G24
C/Genetics:
A/Map position: 5
A/Introns: 53/3; 66/1; 127/2; 177/1; 256/1; 319/2; 361/2; 394/3
A/Note: F13G24.30

Query Match 14.7%; Score 417; DB 2; Length 521;
Best Local Similarity 29.2%; Pred. No. 4.3e-23;
Matches 154; Conservative 68; Mismatches 184; Indels 122; Gaps 24;

QY 75 LSPKLTARLARGSPAYLRFGGTKTDFLFPDKKSTPFRSWSQVQVNDLCKYGSIRP 134
DB 55 LTRPLTKAIKAPKPLRIRIGSLQVQVYDVGNLTKT-----PCR----- 94
QY 135 DVEBKRLRWPYOEQLLREHYOKKFKNS---TYSRSV-----DLYLTFFANCSGLDIF 186
DB 95 -----PFQKM-----NGLRGFSKGCGLMKRWDELNFLTATGAVVTF 132
QY 187 GINALIRTDLQ-----WSSNAQLLDYSSKGYNT-SWELGNEPNSFLKADIFIN 238
DB 133 GINALRGHRLKRGKAMGAMDHINTQDFLNTYVSKGYVIDSWFENLISG--SGVGASVS 190
QY 239 GSQLEBDFIQHLKLRKSTFKNAKLYGPRVGP-----RRKTAKM.KSFLKAGGEVIDSV 293
DB 191 AELVGDLLVLKDVINK-VYKSWLHKPLVLAAGGGEYEOQWYTKLEI---SGPSVADV 246
QY 294 TWHHYVLNGRT--ATREDFLNPVDLDFITSSVQKV---QVVESTRPCKKYLGETSSA 347
DB 247 THHIVYLSGSDNPALVYKIMDPS-----YLSQVSKTKVDVNTQI QHGPASPVGESSGA 302
QY 348 YGGGADLSDTPAAGFMWLDLGLSARWGI EVVMRQVFFGAGNYHLVDE-NEDPLPDYWL 406
DB 303 YNSGGRHVDTFIDSFMYLDQLGMSARHNTKYVCRQLVG-GPYGLLEKGTFFPNDDYS 361
QY 407 SLTFKLVGTGYLMASVQSKRKRLRVYLAHTNTDPRKEDGLTYAINHNTKYL-- 464
DB 362 ALLMRLKMGVLA VOTDGRP--QLRVYAHCSK-----GRAVTLTLNLSQSDFTVS 413
QY 465 -----RLPYFSS--NKQVDKYLRLP---LGPAG--LISKSVOL 495
DB 414 VNSGINVVLNABSRKKKSLDLTLKRPFSWIGSKASGYLNREHYHLTPENGVLRSKTMVL 473
QY 496 NGTLTKMVDQTLPLMEKPLRP-GSSLGLPAFSYFFYIRNAKVAAC 542
DB 474 NKSILKPTATGDI PSL-EPVLSRVNSPLNVLPLSMGFIVLPNPDASAC 520
```

```
RESULT 3
T01953
Hypothetical protein T2L5.6 - Arabidopsis thaliana
C/Species: Arabidopsis thaliana (mouse-ear cress)
C/Date: 26-Feb-1999 #sequence_revision 26-Feb-1999 #text_change 09-Jul-2004
C/Accession: T01953
R/Giesel, C.; Smith, A.; Le, T.
submitted to the EMBL Data Library, October 1998
A/Description: The sequence of A. thaliana T2L5.
A/Reference number: Z14470
A/Accession: T01953
A/Status: translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-190 <GEI>
A/Cross-references: UNIPROT:O82604; EMBL:AF096371; NID:93695386; PID:93695392
A/Experimental source: cultivar Columbia
C/Genetics:
A/Map position: 4
A/Introns: 36/2; 69/3
A/Note: T2L5.6
C/Superfamily: Arabidopsis thaliana hypothetical protein T2L5.6

Query Match 6.0%; Score 169.5; DB 2; Length 190;
Best Local Similarity 27.8%; Pred. No. 2.4e-05;
Matches 54; Conservative 34; Mismatches 57; Indels 49; Gaps 9;

QY 362 ROVPPGAGNYHLVD-ENFDPLPDYWLSLFKKLVGTGYLMASVQSKRKRLRVYLAHTNT 440
DB 12 ROSLIG-GNYGLLNTNFTPNPDYVSALIMRWLMGRKALFTTFSGTK--KIRSYTHCA-- 66
QY 441 DNPYKEDGLTYAINHNV-----TKYLRLLPYPPSKNOVDKYLRPL 483
DB 67 ---ROSKG-ITVLLMLNDNTTIVAKVLELNSFSLRHKHMK-----SYKRASSQLFG-- 115
QY 484 GPHGLL-----SKSVQNLGLTKMVDQTLPLMEKPLRPGSSGLPAFS 528
DB 116 GNGVIGQEEHYHLTKADGNLSQTMNLGNMLQVNSMGDLPRIEPIHINSTRPITAPYS 175
QY 529 YSFFVIRNAKVAAC 542
DB 176 IVFVIMRVNVVPAC 189

RESULT 4
T49648
Hypothetical protein B8B20.20 [imported] - Neurospora crassa
C/Species: Neurospora crassa
C/Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 09-Jul-2004
C/Accession: T49648
R/Schilte, U.; Aign, V.; Hohnsbeil, J.; Brandt, P.; Fartmann, B.; Holland, R.; Nyakatura,
submitted to the Protein Sequence Database, May 2000
A/Reference number: Z25022
A/Accession: T49648
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-2298 <SCH>
A/Cross-references: UNIPROT:Q96U00; EMBL:AL355933; GSPDB:GN00116; NCSP:B8B20.20
A/Experimental source: BAC clone B8B20; strain OR74A
C/Genetics:
A/Gene: NCSP:B8B20.20
A/Map position: 6
A/Introns: 426/3

Query Match 3.9%; Score 112; DB 2; Length 2298;
Best Local Similarity 19.3%; Pred. No. 19;
Matches 114; Conservative 79; Mismatches 190; Indels 208; Gaps 28;

QY 78 PFKLTARGLSPA-----YLRFGGTKTDFLFPDKKSTPFRSWSQV--NQDLC 127
DB 1447 PVDLIERLTIPSNHKEACLINIRANQALRLVVSNGSGASFRPFTIRNNVFNQIID 1506
```

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 23, 2005, 11:19:33 ; Search time 27 Seconds
(without alignments)
1935.026 Million cell updates/sec

Title: SEQ2B
Perfect score: 2841
Sequence: 1 MLRSKPLPPMLLLGP.....LPFSYSPFVIRNAKVAACI 543

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 9621673 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	893.5	31.5	480	2 JC7506	heparanase protein
2	417	14.7	521	2 T45608	hypothetical prote
3	169.5	6.0	180	2 T01953	hypothetical prote
4	112	3.9	2258	2 T49648	hypothetical prote
5	111	3.9	670	2 T10666	hypothetical prote
6	111	3.9	688	2 S32961	hypothetical prote
7	110.5	3.9	356	2 F64383	hypothetical prote
8	107.5	3.8	575	2 T12094	beta-fructofuranos
9	106	3.7	670	2 T38446	microtubule-associ
10	105.5	3.7	411	2 S74760	hypothetical prote
11	105.5	3.7	879	2 E91031	probable outer mem
12	104.5	3.7	788	1 S00652	phosphoribosylamin
13	104	3.7	432	2 F70411	adenylosuccinate s
14	104	3.7	796	2 D70665	transketolase (imp
15	104	3.7	2013	2 A11489	probable peptidogl
16	103.5	3.6	500	2 D87541	beta-xylosidase (l
17	103.5	3.6	676	2 AF1153	transcription anti
18	102	3.6	879	2 F85875	probable fibrinoly
19	102	3.6	897	2 G02529	dynein heavy chain
20	102	3.6	4644	1 A38905	dynein heavy chain
21	101.5	3.6	746	2 T46821	sideophore recept
22	101.5	3.6	746	2 A95420	Rita Rhizobactin r
23	101	3.6	594	2 A82913	hypothetical prote
24	100.5	3.5	604	2 E75119	hypothetical prote
25	100.5	3.5	687	2 F85188	retrotransposon 11
26	100.5	3.5	847	2 AG1001	nitrite reductase
27	100.5	3.5	1314	2 S19488	probable membrane
28	100.5	3.5	1734	2 A41101	phorbol ester-bind
29	100	3.5	578	2 B89045	protein B0238.7 [1

30	100	3.5	654	2 T14202	NADH2 dehydrogenas
31	99.5	3.5	587	2 S36231	beta-fructofuranos
32	99.5	3.5	989	2 AE2140	toxin secretion AB
33	98.5	3.5	629	2 C64180	hypothetical prote
34	98.5	3.5	804	2 G71546	probable DNA gyrase
35	98	3.4	465	2 T19113	hypothetical prote
36	98	3.4	644	2 A97268	methionyl-tRNA syn
37	98	3.4	716	1 C60008	RNA-directed RNA p
38	97.5	3.4	511	2 S61166	probable membrane
39	97	3.4	379	2 A69974	cystathionine gamm
40	97	3.4	437	1 A48061	translational releas
41	97	3.4	726	2 C66085	catalase, hydrotrop
42	97	3.4	726	2 G91237	hydrotropoxidase HP
43	97	3.4	760	2 T34414	hypothetical prote
44	96.5	3.4	510	2 H69893	conserved hypothet
45	96.5	3.4	621	2 A95250	choleline binding pr

ALIGNMENTS

RESULT 1

JC7506
heparanase protein 2a - human
C:/Species: Homo sapiens (man)
C:/Date: 17-Nov-2000 #sequence_revision 17-Nov-2000 #text_change 09-Jul-2004
C:/Accession: JC7506
R:/McKenzie, E.; Tyson, K.; Stamps, A.; Smith, P.; Turner, P.; Barry, R.; Hircock, M.; Pat
Biochem. Biophys. Res. Commun. 276, 1170-1177, 2000
A:/Title: Cloning and expression profiling of Hpa2, a novel mammalian heparanase family me
A:/Reference number: JC7506
A:/Accession: JC7506
A:/Molecule type: mRNA
A:/Residues: 1-480 <MCK>
A:/Cross-references: UNIPROT:O9HB39; GB:AF282885
A:/Comment: This protein, a intracellular membrane-bound enzyme, has biological and therai
Chetraples.
C:/Genetics:
A:/Gene: hpa2a
A:/Map position: 10q23-10q24
C:/Keywords: heparin binding; membrane bound

Query Match	31.5%;	Score 893.5;	DB 2;	Length 480;
Best Local Similarity	35.8%;	Pred. No. 1.4e-58;		
Matches 201;	Conservative 75;	Mismatches 146;	Indels 139;	Gaps 9
QY	20	PLGLPSGAL-----PRPA-----QAQVDVDDPFTQEPPLHVS	55	
DB	18	PPACLPAGALYALALLHLSLSQAGRRPLPVDRAGLKEKTLILLDVSTKAPRVNEN	77	
QY	56	FLSVTIDANLADPRLILGSPKLTTLARGLSPAYLRFQGTQDFLIF---DPKKEST	111	
DB	78	FLSLGLDPSIINH-GWLDPLFSRKRLVTLARGLSPARLFGKRTDPLQONLRNPAKSR-	135	
QY	112	FEERSYQSCOVNODICKYGIIPPDVEEKLRLLEMPYQQLLREHYQKKRKNSTYSSSVD	171	
DB	136	-----GGPGPD-----YYLNKYE-----	148	
QY	172	VLYTFANCSGLDILFGLNMLRLTADLQWNSNAQLLDYCSSKGYNISWELGNEPNSFLK	231	
DB	149	-----DEPNRYT	156	
QY	232	KADIFINGSQLGDFIOLHKLRLK-STFKNAKLYGPDVQOPRRKTKAMLSFLKAGGEVI	290	
DB	157	MHGAIVNSQGLKRYIQKLSLQPIRITRSRSLYGPNIIRPRKNVIALDGMKVAGSTV	216	
QY	291	DSVTMHYYLNGRTAREDFLNDVDLFISSVQKXFQYVESIRPEKRWLGSTSSAYCG	350	
DB	217	DAVTWQHCYIDGRVAVKVMDFLKTRLLDLSDQIRKIQKVVNTYTPGKKIMLEGVTTSG	276	
QY	351	GAPLSDTFAPAGPMWLDKLSARMGIEVVMROVFGAGNYHLDVNSPDLPLPYMISLIF	410	
DB	277	GTMNLSDSYAGFIMLNTLGMLANQSIDIVIRHSFDFGHNLHLDQNFPLPDYMSLILY	336	

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QY 106 PKKESTFEERSYQWQONODICKYGISPPDVEEKLRLMPYQEOILLREHYOKKFKNSY 165
DB 100 -SKENI-----PISCHNCSYKSYPSRLCQ--LIEKPC-----NKKKFLPFIIM 140
QY 166 SRSADVLTYPANCSGLDILFGINALLFTADLQWNSNAQLLDYCSSKGYNISWELGNE 225
DB 141 TGNEMNOIDPCKRTMLKLLFSLNMLRP-NIGMMEKNARELIEFKHKQVAILDQLGNE 199
QY 226 PMSFLKADIFINGSLGDFIQLHKLLRKSTFKNAKLYGPDVGOP--RRKTAKMLKSF 282
DB 200 PMSFGVFNESVTPQILAKDFEKLRLNHNNGYRHSLLVGPDTRPQPHRPPCLKYMIEF 259
QY 283 LAAAGVIVSVTHNYLNGRTATREDPFLNDVLDIFISSVOKPQVVESTPGKKV--M 340
DB 260 LAGSHYIVRSMHQYLLNSKTAKLEDPMWPEFDL---ROQIETMQOTKKYKNIPIW 316
QY 341 LGETSAYGGAPLLSDTFAAGFMWLDKGLSARMGIEVVMROVFFGAGNYHLVDENPD 400
DB 317 LSETSSYGGAGPLGNTYAGSPMLDKGLSAXNISTYIRQSFIG-GYSLVDENLKP 375
QY 401 LPDYMLSLFKKLVGTRVMASVQSSKRRKRLVYHCTNTDNPRYK--GDULTYAIN-- 456
DB 376 LPEMWISVLYKKLVGKVL--QVQCNCSPFORLYIHCTNR--KYNDTSAYVLGYVNL 430
QY 457 -----LHN-----VTXYLRLPYPSNRKQVXYLRLPGHGLSKSVQLNGULT 500
DB 431 MAYARFPLNGTALHGDLLIHEYI-ISAPSNRK-----SKTILLNGWFL 474
QY 501 KMWDDQTLPELMEKPLRPGSSSLGPAFSSYFPIRAXKVAAC 542
DB 475 YV--ESNLHLRPNIRHYGRYVSLPPYSIGFWYIKKTSITVC 514

```

RESULT 15

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Q9SDA1 ID Q9SDA1 PRELIMINARY; PRT; 521 AA.
AC Q9SDA1;
DT 01-MAY-2000 (T-EMBLrel. 13, Created)
DT 01-MAY-2000 (T-EMBLrel. 13, Last sequence update)
DT 01-MAR-2004 (T-EMBLrel. 26, Last annotation update)
DE Hypothetical protein F13G24.30.
OS Name=F13G24.30;
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosid II; Brassicales; Brassicaceae; Arabidopsis.
OC NCBI_TaxID=3702;
RN [1]
RX SEQUENCE FROM N.A.
RA Bevan M., Van Der Schueren J., Chuang Y.J., Voet M., Robben J.,
RA Volckaert G., Bancroft I., Mewes H.W., Lemcke K., Mayer K.F.X.;
RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA EU Arabidopsis sequencing project;
RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL, AL133421, CAB62595.1; -
DR PIR, T45608, T45608.
DR InterPro, IPR005199; Glyco_hydro_79N.
DR InterPro, IPR001254; Peptidase_S1.
DR Pfam, PF03662; Glyco_hydro_79n; 1.
DR PROSITE, PS00135; TRYPSIN_SER; UNKOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 521 AA; 57831 MW; 07D8664A4B305CC2 CRC64;

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Query Match 14.7%; Score 417; DB 2; Length 521;
 Best Local Similarity 29.2%; Pred. No. 7.4e-23;
 Matches 154; Conservative 68; Mismatches 184; Indels 122; Gaps 24;

QY 75 LGSPEKRLTLAGLSFAVYRFGTKTDLIFDPKKESTFEERSYQWQONODICKYGSIPP 134
 DB 55 LTRPLTVAIKAFKPLRIRIGSLQDVIYDVGNLKT-----PCR----- 94

```

QY 135 DVEEKLRLMPYQEOILLREHYOKKFKNS---TYSRSSV-----DVLTPANCSGLDILF 186
DB 95 -----PQCK-----NSGLFGSKGCLHKKRWDELNSFLATGAVTF 132
QY 187 GINALLRTADLQ-----MNSNAQLLDYCSSKGYNI-SWELGENENSLKADIFIN 238
DB 133 GINALRGHRLKRGKAMGAMDHINTQDFLNTYVSKGYVIDSMWFENELSG--SGVGASVS 190
QY 239 GSQIGEDFIQLHKLLRKSTFPNAKLYGPDVGOP-----RRKTAKMLKSFLLAGGEVIDSV 293
DB 191 AELYGKDLVLKDVINK-VTKNSWLHKPILVAFGGFYEQQWYTKLEI---SGPVDVY 246
QY 294 TWHHYLLNGRT--ATREDPFLNDVLDIFISSVQKVF---QVESTRPCKYWLGETSA 347
DB 247 THHIVNLGSDNDPALVKKIMDS-----YLSQVSKTFKDVNQTIOHGGFWASFWVGEISGA 302
QY 348 YGGAPLLSDTFAAGFMWLDKGLSARMGIEVVMROVFFGAGNYHLVDE-NPDPLPDYWL 406
DB 303 YNSGGRHVSDTFLIDFWYLDQLGMSARHNTKYVCHQTLVG-GFYGLLEKGFVPPNDYIS 361
QY 407 SLLPKKLVGTXYLMAVQSSKRRKRLVYHCTNTDNPRYKEGDLTYAINLHNVTXYL-- 464
DB 362 ALLMHRMLGKGVLAVQTDGPP--QLRYAHGSK-----GRAGVTLLILNLSNQDFTVS 413
QY 465 -----RLPYPS---NKQVDKYLRP--LGRHG--LLSKSVOL 495
DB 414 VSGNIVVNLAAESRRKKSLDLDTLKRPFWSIGSKASDGYLNREYHLTPENGVLRSKTYVL 473
QY 496 NGULTKMWDDQTLPELMEKPLRP-GSSSLGPAFSSYFPIRAXKVAAC 542
DB 474 NGSLEKPTATGDI PSL-EPVLRSVNSPLNVLPLSMSTFVLPNPDASAC 520

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Search completed: March 23, 2005, 11:29:35
 Job time : 111.5 secs

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Db 78 FLSLQDPSIIHD-GWLDFLSKRLVTLARGSPAFLRGSKRTDPLQONLRNPAKSRG 136
Qy 112 FEERSYMSQVNODI-----CKYGSIPRVEEKLRLMEYQOQL-LREHYOK 158
Db 137 GGPDPYLYKNKDDIYRSVALDKQCKCIAQ-HRPVMELEQREKAQMLVLLKQF-- 193
Qy 159 KEKNSYSSKSSVAVLYTFANCSCGLDLIFGLNALLRTADLQNMSSNAQLLLDYCSSKGVNI 218
Db 194 ---SNTYS-----NULL-----202
Qy 219 SWELGNENPSFLKKAADIFINGSQLGEDFIQLHKLRLK-STFKNAKLYGPDVGQPRRKTA 277
Db 203 -----TEPNNYRTMHGRAVNGSOLGKDYIQLKSLQPIRISFASLYGNIGRPRKNVIA 257
Qy 278 MLKSLFKAGGEVYDSVTMHYYLNGRTARREDPLNDVLDIFISSVQKYFOVYESRPRK 337
Db 258 LIDGFKKVAGSTVDVATWOHCYIDGKRVKMDFLKTRLDLTSLDDIRKIQKVVNTYTPGK 317
Qy 338 KVMLGETSAYGSGAPULSDTFAGFPMWLDKGLSARMGIEVVMROVFFGAGNYHLVDEN 397
Db 318 KIMLBSVVTTSAGGTNNLSDSYAAGFLWINTLGMLANOGIDVYIRHSFDDHGNHLVDQN 377
Qy 398 FPLPDYWLISLFLKVLGTRKVLMAVQSKRR-----KLRVYLHCTNTDNPRYKEG 448
Db 378 FNPPLDPMYLSLYKRLIGPKVLAVHVAQLQKRPGRVIRDKLRIRYAHCTNNHNNHYRAG 437
Qy 449 DLTVAIINAHNTKYRLPYPPSNKQVDXYLRLPGPHGLSKSVQNLGLTKMVDQTL 508
Db 438 STLFPLINHRSRKIKLGLTRDKLVHGYLLQPYQOEGLSKSKSVQNLQPLVMVDGTL 497
Qy 509 PLMEKPLRPGSSGLGPAFYSFFVIRNAKVAAC 542
Db 498 PELKRPRLRAGRTLVIPVYTMGFVVKNNALAC 531

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RESULT 13

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Q9HB39 PRELIMINARY; PRT; 480 AA.
ID 09HB39
AC 09HB39;
DT 01-MAR-2001 (TEMBLrel. 16, Created)
DT 01-MAR-2001 (TEMBLrel. 16, Last sequence update)
DT 01-MAR-2004 (TEMBLrel. 26, Last annotation update)
DE Heparanase-like protein HP2a.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
OC NCBI_TaxID=9606;
OX NCBI_TaxID=9606;
RN RP
RX SEQUENCE FROM N.A.
RX MEDLINE=20483645; PubMed=11027606; DOI=10.1006/dbrc.2000.3586;
RA McKenzia E., Tyson K., Stamps A., Smith P., Turner P., Barry R.,
RA Hitecock M., Patel S., Barry B., Stuberfield C., Tetreault J., Page M.;
RT "Cloning and expression profiling of Hpa2, a novel mammalian
RL heparanase family member.";
RL Biochem. Biophys. Res. Commun. 276:1170-1177(2000).
RN RP
RX SEQUENCE FROM N.A.
RX McKenzia E.A., Tyson K., Stamps A.;
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB282885; AAG23421.1; -.
DR PIR; JC7506;
DR InterPro; IPR005199; Glyco_hydro_79N.
DR Pfam; PR03662; Glyco_hydro_79n; I.
SQ SEQUENCE 480 AA; 5390 MW; F75F89F67AC1FF83 CRC64;

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Query Match 31.5%; Score 893.5; DB 2; Length 480;
 Best Local Similarity 35.8%; Pred. No. 5,1e-59;
 Matches 201; Conservative 75; Mismatches 146; Indels 139; Gaps 9;

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Qy 20 PLGPIUSPGL-----RPPA-----QAQVVDLDFIQEQLHVSRS 55
Db 18 PACIAPGALYALLLHLISLISQAGDRRLPVDRAAGLKEKTLILLDVSTKPNVKTVEN 77

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Qy 56 FLSVTIDANLATDPRFLILGSPKLTTLARGSPAVLRFEGTKTDFLIF----DPKKEST 111
Db 78 FLSLQDPSIIHD-GWLDFLSKRLVTLARGSPAFLRGSKRTDPLQONLRNPAKSR- 135
Qy 112 FEERSYMSQVNODICTKGSIPPDVEEKLRLMEYQOQLLREHYOKRKNSYSSSDV 171
Db 136 -----GGPDP-----YYLKNE-----148
Qy 172 VLYTFANCSCGLDLIFGLNALLRTADLQNMSSNAQLLLDYCSSKGVNISWELGNENPSFLK 231
Db 149 -----DEPNNYRT 156
Qy 232 KADIFINGSQLGEDFIQLHKLRLK-STFKNAKLYGPDVGQPRRKTAKMLKSPKAGGEVY 290
Db 157 MHGRAVNGSOLGKDYIQLKSLQPIRISFASLYGNIGRPRKNVIALIDGFKKVAGSTV 216
Qy 291 DSVTMHYYLNGRTARREDPLNDVLDIFISSVQKYFOVYESRPRKRYWLGETSAYGG 350
Db 217 DAVTWOHCYIDGRVVKVMDFLKTRLDLTSLDDIRKIQKVVNTYTPGKKTWLGCVVTSAG 276
Qy 351 GAPLSDTFAGFPMWLDKGLSARMGIEVVMROVFFGAGNYHLVDENFPLPDYWLISLF 410
Db 277 GTNNLSDSYAAGFLWINTLGMLANOGIDVYIRHSFDDHGNHLVDQNEPPLDPMYLSLY 336
Qy 411 KLVGTRKVLMAVQSKRR-----KLRVYLHCTNTDNPRYKEGDLTLVAIINAHNT 461
Db 337 KRLIGPKVLAVHVAQLQKRPGRVIRDKLRIRYAHCTNNHNNHYRAGSTLFLINHRSR 396
Qy 462 KYRLPYPPSNKQVDXYLRLPGPHGLSKSVQNLGLTKMVDQTLPLMEKPLRPGSS 521
Db 397 KXIKLAGTRDKLVHGYLLQPYQOEGLSKSKSVQNLQPLVMVDGTLPELKRPRLRAGRT 456
Qy 522 LGHPAFYSFFVIRNAKVAAC 542
Db 457 LVIPVYTMGFVVKNNALAC 477

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RESULT 14

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O8T108 PRELIMINARY; PRT; 515 AA.
ID O8T108
AC O8T108;
DT 01-JUN-2002 (TEMBLrel. 21, Created)
DT 01-JUN-2002 (TEMBLrel. 21, Last sequence update)
DT 05-JUL-2004 (TEMBLrel. 27, Last annotation update)
DE Heparanase-like protein.
GN Name=Bmhepa.
OS Bombyx mori (Silk moth).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Bombycoidea;
OC Bombycidae; Bombyx.
OX NCBI_TaxID=7091;
RN RP
RX SEQUENCE FROM N.A.
RX STRAIN=D50; TISSUE=Posterior silkgland;
RA Koike Y., Mita K., Suzuki M.G., Maeda S., Abe H., Osoegawa K.,
RA deJong P.J., Shimada T.;
RT "Genomic sequence of a 320-kb segment of the Z chromosome of Bombyx
RL mori containing a kettin ortholog.";
RL Mol. Genet. Genomics 269:137-149(2003).
DR EMBL; AB079860; BAB85191.1; -.
DR EMBL; AB090307; BAC10612.1; -.
DR InterPro; IPR005199; Glyco_hydro_79N.
DR Pfam; PR03662; Glyco_hydro_79n; I.
SQ SEQUENCE 515 AA; 59769 MW; FB8100AB86EDDADB CRC64;

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Query Match 24.6%; Score 699; DB 2; Length 515;
 Best Local Similarity 35.2%; Pred. No. 3,1e-44;
 Matches 184; Conservative 82; Mismatches 182; Indels 74; Gaps 18;

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Qy 46 QEPHLHVSFSLVTIDANLATDPRFLILGSPKLTTLARGSPAVLRFEGTKTDFLIFD 105
Db 42 QEDIKLISEDFLSGID-TIETENYNNRINYSDTRLELAALSPARLRUGTWSERLIF- 99

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QY 20 PLGLPSFGAL-----PRPA-----QAQDVVDLDFTOEBPLHVS 55
| : : : : :
DB 18 PRACIAPGALYLLALLHLSTSSQAGDRRLPVDRAGLKEKTLILLDVSTKNPVRTNEN 77
QY 56 FLSTVTDANLATDPRFLIILGSPKLTARGLSPAYLRFGGTDTDLIF----DPKKEST 111
| : : : : :
DB 78 FLSTLODPSI IHD-GWLDFLSSKRLVTLARGLSPAYLRFGGTDTDLIFONTLNPAKSRG 136
QY 112 FEERSYQOVNODI-----CKYGSIPPEVEEKLRLWEPYQOL-LYREHYOK 158
| : : : : :
DB 137 GGGPDYLYKKNEDIVRSVDALDKQCKIAQ-HPDWMELQREKAAQHLVLLKQFEN 195
QY 159 KERNSTYSSSVVDVLYTFANCSGLDIFGLNALLRADLOWNSSNAQLLDYSSKGYNI 218
| : : : : :
DB 196 TYSNLILTLARSLDKLYNSADCSGLHLIFALNALRRPNNSMSSSALILKYASKKYNI 255
QY 219 SWEIENEPSPFLKADIFINGSQGEDFIQHLKLR-STFKNAKLYGPDVQPRKRTAK 277
| : : : : :
DB 256 SWEIENEPNNYRTMHGRAVNSQLGKDYIQKSLQPIRISYRASLYGPNGPRKNVIA 315
QY 278 MLKSPFLKAGEVIDSVTWHYYLNGRTATREDPLNDVLDIFISSVQKVFQVESTREPGK 337
| : : : : :
DB 316 LLDGFKVAGSTYDATTWQHICYIDGRVVKMBFLKRLDITLSDQIRKIQKVNVTYTPGK 375
QY 338 KVMIGETSSAYGGAPILSDTPAAGFMWLDKGLSARMGIEVVRQVFGAGNYHVDEN 397
| : : : : :
DB 376 KTWLBEVVTTSAGGTNNLSDSYAAGFLMNTLGLANOGIDVYIRHSFHDGYNHLVDQN 435
QY 398 FDBLPYVWLSLFPKLVGTGVYKVMASVQSKRR-----KLRVYLHCNTNTPRYKKG 448
| : : : : :
DB 436 FDBLPYVWLSLFPKLVGTGVYKVMASVQSKRR-----KLRVYLHCNTNTPRYKKG 495
QY 449 DTLVYINLHNVYKYLRLPYFENKQVDKYLRLPGHGLSKSVQNLGTLKAVDDQL 508
| : : : : :
DB 496 SITLFLINLHRSKKIKLACTLRDKLVHQYLLQPYQGBGLKSVQNLGTLKAVDDQL 555
QY 509 PPLMEKPLRPGSSGLPAPSYFFVIRNAKVAAC 542
| : : : : :
DB 556 PELKPRPLRAGRTLVPVTMGFFVNVNVALAC 589

RESULT 11
Q8WMQ1 PRELIMINARY; PRT; 548 AA.
ID 08WMQ1;
AC 08WMQ1;
DT 01-MAR-2002 (T-EMBLrel. 20, Created)
DT 01-MAR-2002 (T-EMBLrel. 20, Last sequence update)
DT 01-JUN-2003 (T-EMBLrel. 24, Last annotation update)
DE Hepatanase 3.
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Prostate;
RA Legoux P., Legoux R., O'Brien D., Salome M.;
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Prostate;
RA Pessague Salontas B.J.O.P.S.;
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: A0299720; CAC82492.1; -
DR Pfam: PF03662; Glyco_hydro_79n; 1.
SQ SEQUENCE 548 AA; 61771 MW; B8986303FC73A60A CRC64;

Query Match 35.6%; Score 1011.5; DB 2; Length 548;
Best Local Similarity 41.6%; Pred. No. 7.1e-68;
Matches 223; Conservative 80; Mismatches 180; Indels 53; Gaps 9;

QY 8 ALPPLMLLLGLPLSPGAL-----PRPA-----QAQDVVDLDF 43
| : : : : :

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DB 6 APPEAMLSNRRPACIAPGALYLLALLHLSTSSQAGDRRLPVDRAGLKEKTLILLDV 65
QY 44 FTOEPHLTVSPFLSVTIDANLATDPRFLIILGSPKLTARGLSPAYLRFGGTDTDLIF 103
| : : : : :
DB 66 STKNPVRTNENFLSQDPSI IHD-GWLDFLSSKRLVTLARGLSPAYLRFGGTDTDLIF 124
QY 104 F----DPKKESTFEERSYQOVNODI-----CKYGSIPPEVEEKLRLWEPYQ 147
| : : : : :
DB 125 FQMLRNPAPKSRGGPGPDYLYKKNEDIVRSVDALDKQCKIAQ-HPDWMELQREKAAQ 183
QY 148 EQL-LYREHYOKKFNKSTYSSSVVDVLYTFANCSGLDIFGLNALLRADLOWNSSNAQL 206
| : : : : :
DB 184 MHLVLKEQPSNTSYLLILARSLDKLYNSADCSGLHLIFALNALRRPNNSMSSSALS 243
QY 207 LLDYSSKGYNISWEIENEPNNYRTMHGRAVNSQLGKDYIQKSLQPIRISYRASLYG 265
| : : : : :
DB 244 LKYSASKKYNISWEIENEPNNYRTMHGRAVNSQLGKDYIQKSLQPIRISYRASLYG 303
QY 266 PDVQPRKRTAKMLKSLKAGEVIDSVTWHYYLNGRTATREDPLNDVLDIFISSVQK 325
| : : : : :
DB 304 PNIGRPRKNVIALLDGFMKVAGSTVDATWQHICYIDGRVVKMBFLKRLDITLSDQIRK 363
QY 326 VPQVVESTRPGKVMIGETSSAYGGAPILSDTPAAGFMWLDKGLSARMGIEVVRQV 385
| : : : : :
DB 364 IQKVNVTYTPGKKTWLEGVVTSAGGTNNLSDSYAAGFLMNTLGLANOGIDVYIRHSF 423
QY 386 FGAAGNYHVDENEDPLDYWLSLFPKLVGTGVYKVMASVQSKRR-----KLRVYLH 436
| : : : : :
DB 424 FHDGYNHLVDQNPLPDYWLSLFPKLVGTGVYKVMASVQSKRR-----KLRVYLH 483
QY 437 CTNTDNPYKEDLTLVAINLHNVYKYLRLPYFENKQVDKYLRLPGHGLSKSVQNLGTL 492
| : : : : :
DB 484 CTNNHNNHNVYKSLTFLINLHRSKKIKLACTLRDKLVHQYLLQPYQGBGLKSKT 539

RESULT 12
Q9HB38 PRELIMINARY; PRT; 534 AA.
ID Q9HB38;
AC Q9HB38;
DT 01-MAR-2001 (T-EMBLrel. 16, Created)
DT 01-MAR-2001 (T-EMBLrel. 16, Last sequence update)
DT 01-MAR-2004 (T-EMBLrel. 26, Last annotation update)
DE Hepatanase-like protein Hpa2b.
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20483645; PubMed=11027606; DOI=10.1006/bbrc.2000.3586;
RA McKenzie E., Tyson K., Stamps A., Smith P., Turner P., Barry R.,
RA Hircok M., Patel S., Barry E., Stuberfield C., Terrett J.,
RT "Cloning and expression profiling of Hpa2, a novel mammalian
hepatanase family member.";
RL Biochem. Biophys. Res. Commun. 276:1170-1177(2000).
RN [2]
RP SEQUENCE FROM N.A.
RA McKenzie E.A., Tyson K., Stamps A.;
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF282886; AAC23422.1; -
DR InterPro: IPR005199; Glyco_hydro_79n.
DR Pfam: PF03662; Glyco_hydro_79n; 1.
SQ SEQUENCE 534 AA; 60063 MW; C3DE5E900CB338C4 CRC64;

Query Match 32.8%; Score 932.5; DB 2; Length 534;
Best Local Similarity 37.6%; Pred. No. 6.6e-62;
Matches 216; Conservative 79; Mismatches 168; Indels 111; Gaps 12;

QY 20 PLGLPSFGAL-----PRPA-----QAQDVVDLDFTOEBPLHVS 55
| : : : : :
DB 18 PRACIAPGALYLLALLHLSTSSQAGDRRLPVDRAGLKEKTLILLDVSTKNPVRTNEN 77
QY 56 FLSTVTDANLATDPRFLIILGSPKLTARGLSPAYLRFGGTDTDLIF----DPKKEST 111
| : : : : :

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Matches 321; Conservative 86; Mismatches 114; Indels 11; Gaps 3;

QY 13 LMLLLGLPLSPALPRPAQADVDDLFQOEPHLVSPFLSVTIDANLAPRRL 72
 Db 2 LVLHLLVLLAVP-----RTAEQLGREPIGAVSPFLSLTIDASLARDPRV 52

QY 73 ILLGSPKLTTLARGLSPAYLRFEGTKTDLIPDPKKESTFEERSYQSOVNODICKYGS1 132
 Db 53 ALLRHPKHTLASGLSPGLRFGSTDTLIPNKNOSTWEKVLSEFQA-KDVCAMPS 111

QY 133 PRDVEEKLLEMPYQQLLREHYQKFKFQSTYSRSVLYTFPANGSLDLIFGLNALL 192
 Db 112 FAVVPLLTQWPLQDEKLLEHSHWKKHQTITRSTLDLHTFASSSGFRLVFGINALL 171

QY 193 PRADLOMNSNQLLDYCSKGVN1SWEIGNEPNSFLKKADIFINGSQLGEDFIQHLK 252
 Db 172 PRAGLOMDSNKKQLGYCAORSYN1SWEIGNEPNSFRKKSGLCIDFGQGRDFVLRQL 231

QY 253 L-RKSTFNKAKLYGPDVQGPRRKTAFLKAGGEVIDSVTMHYLYNGRTATREDEL 311
 Db 233 LSGHPLRYRAELYGLDVQPRKHTOHLRSPKSGKALDSVTWHYLYNGRSATREDEL 291

QY 312 NPDVDLDFISSVQKFOVVESTRPKKWLGETSSAYGGAPLISDTFAAGFMWLDKGL 371
 Db 292 SPEVLDSFYATAIHDVIGIVEATVPGKKWLGETGSAVGGAPQLSNTYVAGFMWLDKGL 351

QY 372 SARMGIEVVMROVFFGAGNYHLVDENFDLPDYWLSLFRKLVGTVMASVQSGRRKL 431
 Db 352 AARRGIDVMKROVSFGAGSYHLVDAGFKPLPDYWSLTKRLVGLRVLOASVQADARRP 411

QY 433 RYVLTHTNTDNPYKEGDLTYA1N1LHNTKYLRLEPPSNKQVDKYLRLPLGPHGLSK 491
 Db 412 RYVLTHTNRPYKRGDVTLPALNLSNTQSLQPKQWMSKVDQYLLPHGKDSILSR 471

QY 492 SYQLNGLTAKVDDOTLPRLMEKPLRPGSSGLPAPSYGFFVIRNAKVAACI 543
 Db 472 EYQLNGRLQVDDDTLPALHEMALPAGSTGLPAPSYGFFVIRNAKVAACI 523

RESULT 9
 Q9HB37 PRELIMINARY; PRT; 592 AA.

AC Q9HB37;
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Heparanase-like protein HP42C.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20483645; PubMed=11027606; DOI=10.1006/birc.2000.3586;
 RA McKenzie E., Tyson K., Stamps A., Smith P., Turner P., Barry R.,
 RA Hircock M., Patel S., Barry E., Stubberfield C., Terrett J., Page M.;
 RT "Cloning and expression profiling of Hpa2, a novel mammalian
 RT heparanase family member";
 RL Biochem. Biophys. Res. Commun. 276:1170-1177(2000).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA McKenzie E.A., Tyson K., Stamps A.;
 RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AR282887; AAC23423.1; -
 DR GO; GO:0005622; C:intracellular; TAS.
 DR GO; GO:0030305; F:heparanase activity; TAS.
 DR InterPro; IPR005199; Glyco_hydro_79N.
 DR Pfam; PF03662; Glyco_hydro_79n; 1.
 SQ SEQUENCE 592 AA; 66580 MW; 95C384AD9A74258B CRC64;

Query Match 40.5%; Score 1150.5; DB 2; Length 592;
 Best Local Similarity 43.4%; Pred. No. 2.3e-78;
 Matches 249; Conservative 83; Mismatches 189; Indels 53; Gaps 9;

QY 20 PLGLSPGAL-----PRPA-----QAQDVDDLFQOEPHLVSPS 55
 Db 18 PRACIAPGALYVALLHLHLSLSQAGDRRLPVDRAGLKEKTLILLDVSTKNPVRVNN 77

QY 56 FLSTVIDANLADPRFLILGSPKRTTLARGLSPAYLRFEGTKTDLIF----DPKKEST 111
 Db 78 FLSLQDPSI1HD-GWLDPLSSKRLVTLARGLSPAYLRFEGTKTDLIFQONLRNPKSSRG 136

QY 112 FEERSYQSOVNODI-----CKYGS1PRDVEEKLLEMPYQQL-LLRHYQK 158
 Db 137 GGPDDYLYNNYDDIVRSVDALDKQCKIAO-HPVMLELQREKAAQHLVLKQFSN 195

QY 159 KFKNSYSSRSYDVLYTFPANGSGDLIFGLNALLRTADLOMNSNQLLDYCSKGVN1 218
 Db 196 TYSNLTITARSIDKLYNFADCSGLHIFPLNLRNPNNSWSSSLTKTSASKKYN1 255

QY 219 SWEIGNEPNSFLKKADIFINGSQLGEDFIQHLKLRK-STFNKAKLYGPDVQGPRRKTA 277
 Db 256 SWEIGNEPNNRYTMHGRAVNGSQLGKDYIQLKSLQPIRIYSRASLYGNIGRPRKNVLA 315

QY 278 MLKSPKAGGEVIDSVTMHYLYNGRTATREDELFPDVLDFISSVQKFOVVESTRPK 337
 Db 316 LLDGFKAAGSTVDATWQHCVYIDGRVVKMDPLKTRLLDTLSDOIQRKIQKVNTYTPGK 375

QY 338 KYWLGETSAYGGAPLISDTFAAGFMWLDKGLSARMGIEVVMROVFFGAGNYHLVDEN 397
 Db 376 KTWLBEVYTSAGGNTNLSDSYAGFLWANTGTGMLANOSIDVYIRHSFDDHGYNHLYDQ 435

QY 398 FDPPLDYWSLFLFKLVGTVMASVQSGRR-----KLVYVLTHTNTDNPYKEG 448
 Db 436 FVPLPDYWSLTKYRLIGPKVLAHVAGQRKPRPRVIRDKLRIYAHCTNNHNNHYVAG 495

QY 449 DLTVA1N1LHNTKYLRLEPPSNKQVDKYLRLPLGPHGLSKVQNLTLKMDVDTL 508
 Db 496 STLFITN1HRSRKIKIAGLRDKLVHQLYLPQYQBELKSKSVQNLQPLVMVDDGTL 555

QY 509 PLMEKPLRPGSSGLPAPSYGFFVIRNAKVAAC 542
 Db 556 PELKRPRLPAGRTIVPPTMGFFVVKVNNALAC 589

RESULT 10
 O8WMQ2 PRELIMINARY; PRT; 592 AA.

AC O8WMQ2;
 DT 01-MAR-2002 (TrEMBLrel. 20, Created)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Heparanase 2.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX TISSUE=Prostate;
 RA Legoux P., Legoux R., O'Brien D., Salome M.;
 RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Prostate;
 RA Peseque Safontas B.J.O.P.S.;
 RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AJ299719; CAC82491.1; -
 DR GeneW; HGNC:18374; HPS2.
 DR Pfam; PF03662; Glyco_hydro_79n; 1.
 SQ SEQUENCE 592 AA; 66520 MW; 9478841FEACD558B CRC64;

Query Match 40.2%; Score 1142.5; DB 2; Length 592;
 Best Local Similarity 43.2%; Pred. No. 9.4e-78;
 Matches 248; Conservative 83; Mismatches 190; Indels 53; Gaps 9;

[illegible]

DR	EMBL: AF184967: AAP04563.1; '-'	DR	InterPro: IPR005199; Glyco_hydro_79N	DR	Pfam: PF03662; Glyco_hydro_79n; I	DR	SEQUENCE	536 AA; 60568 MW; 620861PF9EE28421 CRC64;
Query Match	74.8%; Score 2126; DB 2; Length 536;							
Best Local Similarity	75.8%; Pred. No. 2,4e-152;							
Matches	406; Conservative 50; Mismatches 79; Indels 0; Gaps 0;							
QY	9 LPPPLMLLLGPGLPSPGALPRPAQADVDVDDLFFQOEPLHLVSPSELSVTIDANLATD	68						
DB	2 LRPILLMLMWRLMALQGTTPAGTAPTKDDVDLEFYTKRLQFSVPSFLSTIDASLATD	61						
QY	69 PRFLILGSPGLRTLAGLSPAYRFEGGTGKIDFLIPPKESTPEERSYMQQVNOIDCK	128						
DB	62 PRFLITFLGSPPLRLALAGLSPAYLRFGGTKIDFLIPPKKPTSEERSYMQQONNDICG	121						
QY	129 YGSIIPDVEEKLRLWEPYOEOLLIREHYQKKFKKSTSRSSVDVLVTPANCSGDLIFGL	188						
DB	122 SERVSADVRLKIQEMEPFQELLRLREQYQREFKNSTYSRSSVDMLYSPAKCSRIDLIFGL	181						
QY	189 NALLRTDLDQNNSSNAOLLIDYCSKGNISMEIGNEPNSLTKADIFINGSQLGEDFIQ	248						
DB	182 NALLRTDPLRLNNSSNAOLLINVCSSKGNISMEIGNEPNSLTKAQAQISIDSLQGEDPVE	241						
QY	249 LHLKLRSKTFPKNAKLYGPDVGPQPRKTKAKMLKSLKAGGEVIDSVTHHHYLYNGRTATRE	308						
DB	242 LHLKLQSAFQNAKLYGPDIGQPRGKTKVLRSLFKAGGEVIDSLTWHHHYLYNGRVATKE	301						
QY	309 DFLNPDVLDTISSYQKLFQVVESTRPCKKYWLGETSSAYGGGAPLISDFPAAGFMWLDX	368						
DB	302 DFLSSDVLDTFLISYQKLIKVKTKEMTPCKKWLGETSSAYGGGAPLISNTTAAAGFMWLDX	361						
QY	369 LGLSARMGIEVVMQVFPFGAGNYHLVDENPDLPDPYMLSLLFKKLVGTKVLMAVSQSKR	428						
DB	362 LGLSQQLGIEVVMQVFPFGAGNYHLVDENPEPLPDYMLSLLFKKLVGPKVLMSEKVGDR	421						
QY	429 RKLRYVHCTNDNPRYKSGDLYTALNLHWTKYLRPYPFSSKQVNDXYLLRPLGPHGL	488						
DB	422 SKLRVYHCTNYVHRYREGDLYTVALNLHWTKYLRPPMFPSVVDKYLKLPKPGSGGL	481						
QY	489 LSKSVQLNGLTLKAWDDQTLPLMEKPLPPSSSLGLPAFSYFVYIRNAKYAACT 543							
DB	482 LSKSVQLNGLTLKAWDDQTLPLMEKPLPPASSSLSVPAFSYGFYIRNAKIACI 536							
RESULT 8								
Q90YK5	PRELIMINARY; PRT; 523 AA.							
AC	Q90YK5:							
DT	01-DEC-2001 (TREMBLrel. 19, Created)							
DT	01-DEC-2001 (TREMBLrel. 19, Last sequence update)							
DT	01-JUN-2002 (TREMBLrel. 21, Last annotation update)							
DE	Heparanase.							
OS	Gallus gallus (Chicken).							
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;							
OC	Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;							
OX	Gallus.							
OX	NCBI_TaxID=9031;							
RP	SEQUENCE FROM N.A.							
RX	MEDLINE=21369959; PubMed=11387326; DOI=10.1074/jbc.M102462200;							
RA	Goldsmith O., Zcharia E., Ainsom H., Guatta-Rangini Z., Atzmon R.,							
RA	Michal I., Pecker I., Mitrani E., Vlodavsky I.;							
RT	"Expression pattern and secretion of human and chicken heparanase are							
RT	determined by their signal peptide sequence."							
RL	J. Biol. Chem. 276:29178-29187(2001).							
DR	EMBL: AY037007; AAK82648.1; '-'							
DR	Pfam: PF03662; Glyco_hydro_79n; 1.							
SO	SEQUENCE 523 AA; 58386 MW; 8E80B7B18C9BE881 CRC64;							
Query Match	58.0%; Score 1648.5; DB 2; Length 523;							
Best Local Similarity	60.3%; Pred No. 3.5e-116;							

RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohnato N., Okazaki Y.,
 RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
 RA Sasaki D., Shibata K., Shingawa A., Shiraki T., Sogabe Y., Tagami M.,
 RA Tagawa A., Takahashi F., Takaku-Akahita S., Takeda Y., Tanaka T.,
 RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.,
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
 RN [8]
 RP SEQUENCE FROM N.A.
 RC STRAIN=JUL/J; TISSUE=Spleen;
 RA Hulett M.D., Wang J., Hornby J.R., Freeman C., Pagler E., McHenry J.,
 RA Hulett M.D., Wang J., Hornby J.R., Freeman C., Pagler E., McHenry J.,
 RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY077467; AAL76083.1; -
 DR EMBL; AK040471; BAC30600.1; -
 DR EMBL; AF359507; AA015188.1; -
 DR MGD; MGI:1343124; Hspc.
 DR GO; GO:0005578; C:extracellular matrix (sensu Metazoa); TAS.
 DR InterPro; IPR005199; Glyco_hydro_79N.
 DR Pfam; PF03662; Glyco_hydro_79n; 1.
 SQ SEQUENCE 535 AA; 60065 MW; 6E7A8302FB8A0DF CRC64;

Query Match 75.8%; Score 2153; DB 2; Length 535;
 Best Local Similarity 76.8%; Pred. No. 2.1e-154;
 Matches 408; Conservative 50; Mismatches 73; Indels 0; Gaps 0;

QY 13 LMLLLGPIGPSLPPAQAQVVDLDFPTQEPHLVSPFLSVITIDANLATDPRFL 72
 DB 5 LLLMLGPIGALAQAPACTAPDDVDLEFYTKRLRSVSPFLSITIDASLATDPRFL 64
 QY 73 ILLGSPKRTTLARGSPAYLRFQGTGTDPLFDPKKESFTEERSYQWQOVNODICKYGS 132
 DB 65 TFLGSPRLALARGSPAYLRFQGTGTDPLFDPKKESFTEERSYQWQOVNODICKYGS 124
 QY 133 PDVBEKRLLEMPYQOQLLREHYQKKEFNSTYSRSSVDVLYTFANCSGLDILFGINALL 192
 DB 125 SAAVLRKLQVEMPFOELLRLREQYQKEFNSTYSRSSVDVLYTFANCSGLDILFGINALL 184
 QY 193 RTADIQWNSNAQLLDYSSKGYNISWEIGNEPNFLKKAADIFINGSQLGDFIOLHKL 252
 DB 185 RLPDLRMNSNAQLLDYSSKGYNISWEIGNEPNFLKKAADIFINGSQLGDFIOLHKL 244
 QY 253 LRKSTFKNAKLYGPDVGQPRRTAKMLKSLFKAAGEVIDSVTHHYLYNGRTATREDPLN 312
 DB 245 LQSAFQNAKLYGPDVGQPRRTAKMLKSLFKAAGEVIDSVTHHYLYNGRTATREDPLN 304
 QY 313 PVDLFISSVQKVPVQVSTPRGKVMWLGETSASAYGGAAPLLSDTFAAGFMWLDKLGIS 372
 DB 305 SDVLDLFISSVQKILKVTKEITPGKKVMWLGETSASAYGGAAPLLSDTFAAGFMWLDKLGIS 364
 QY 373 ARMGIEVVMKQVFPFAGNHYLDENFPLPDYWLSTLFFKLVGTGYLMASVQSKRRKL 432
 DB 365 AQMGIEVVMKQVFPFAGNHYLDENFPLPDYWLSTLFFKLVGTGYLMASVQSKRRKL 424
 QY 433 VYLHCTNTDNPYKSGDLTLVYLNHNVTKYRLPYPFSENKQVQDKYLRLPLGPHGLSKS 492
 DB 425 VYLHCTNVNHPYKSGDLTLVYLNHNVTKYRLPYPFSENKQVQDKYLRLPLGPHGLSKS 484
 QY 493 VOLNGILTKMVDQTLPLMEKRLRPGSSGLPARYSPFVIRNAKVAACI 543
 DB 485 VOLNGILTKMVDQTLPLMEKRLRPGSSGLPARYSPFVIRNAKVAACI 535

RESULT 5
 Q6Y6Z1 PRELIMINARY; PRT; 535 AA.
 ID Q6Y6Z1
 AC Q6Y6Z1
 DT 05-JUL-2004 (TREMBlrel. 27, Created)
 DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
 DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
 DE Heparanase.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22841152; PubMed=12837765; DOI=10.1074/jbc.M300925200;
 RA Gong F., Jemth P., Galvis M.L.E., Vlodaysky I., Horner A., Lindahl U.,
 RA Li J.P.,
 RT "Processing of macromolecular heparin by heparanase."
 RL J. Biol. Chem. 278:35152-35158(2003).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Li J.-P., Gong F., Lindahl U.,
 RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY151051; AAM41636.1; -
 DR GO; GO:0005578; C:extracellular matrix (sensu Metazoa); TAS.
 DR InterPro; IPR005199; Glyco_hydro_79N.
 DR Pfam; PF03662; Glyco_hydro_79n; 1.
 SQ SEQUENCE 535 AA; 59992 MW; 3748ABE3795C718A CRC64;

Query Match 75.4%; Score 2143; DB 2; Length 535;
 Best Local Similarity 76.8%; Pred. No. 1.2e-153;
 Matches 408; Conservative 49; Mismatches 74; Indels 0; Gaps 0;

QY 13 LMLLLGPIGPSLPPAQAQVVDLDFPTQEPHLVSPFLSVITIDANLATDPRFL 72
 DB 5 LLLMLGPIGALAQAPACTAPDDVDLEFYTKRLRSVSPFLSITIDASLATDPRFL 64
 QY 73 ILLGSPKRTTLARGSPAYLRFQGTGTDPLFDPKKESFTEERSYQWQOVNODICKYGS 132
 DB 65 TFLGSPRLALARGSPAYLRFQGTGTDPLFDPKKESFTEERSYQWQOVNODICKYGS 124
 QY 133 PDVBEKRLLEMPYQOQLLREHYQKKEFNSTYSRSSVDVLYTFANCSGLDILFGINALL 192
 DB 125 SAAVLRKLQVEMPFOELLRLREQYQKEFNSTYSRSSVDVLYTFANCSGLDILFGINALL 184
 QY 193 RTADIQWNSNAQLLDYSSKGYNISWEIGNEPNFLKKAADIFINGSQLGDFIOLHKL 252
 DB 185 RLPDLRMNSNAQLLDYSSKGYNISWEIGNEPNFLKKAADIFINGSQLGDFIOLHKL 244
 QY 253 LRKSTFKNAKLYGPDVGQPRRTAKMLKSLFKAAGEVIDSVTHHYLYNGRTATREDPLN 312
 DB 245 LQSAFQNAKLYGPDVGQPRRTAKMLKSLFKAAGEVIDSVTHHYLYNGRTATREDPLN 304
 QY 313 PVDLFISSVQKVPVQVSTPRGKVMWLGETSASAYGGAAPLLSDTFAAGFMWLDKLGIS 372
 DB 305 SDVLDLFISSVQKILKVTKEITPGKKVMWLGETSASAYGGAAPLLSDTFAAGFMWLDKLGIS 364
 QY 373 ARMGIEVVMKQVFPFAGNHYLDENFPLPDYWLSTLFFKLVGTGYLMASVQSKRRKL 432
 DB 365 AQMGIEVVMKQVFPFAGNHYLDENFPLPDYWLSTLFFKLVGTGYLMASVQSKRRKL 424
 QY 433 VYLHCTNTDNPYKSGDLTLVYLNHNVTKYRLPYPFSENKQVQDKYLRLPLGPHGLSKS 492
 DB 425 VYLHCTNVNHPYKSGDLTLVYLNHNVTKYRLPYPFSENKQVQDKYLRLPLGPHGLSKS 484
 QY 493 VOLNGILTKMVDQTLPLMEKRLRPGSSGLPARYSPFVIRNAKVAACI 543
 DB 485 VOLNGILTKMVDQTLPLMEKRLRPGSSGLPARYSPFVIRNAKVAACI 535

RESULT 6
 Q7IRP1 PRELIMINARY; PRT; 536 AA.
 ID Q7IRP1
 AC Q7IRP1
 DT 05-JUL-2004 (TREMBlrel. 27, Created)
 DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
 DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
 DE Heparanase.
 GN Name=Hspc;
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]

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RESULT 3
Q9MYXO PRELIMINARY; PRT; 545 AA.
ID 09MYXO
AC 09MYXO;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Heparanase.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovinae; Bos.
OC NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Placenta;
RX MEDLINE=21176669; PubMed=1127877;
RA Kizaki K., Nakano H., Nakano H., Takahashi T., Imai K., Hashizume K.;
RT "Expression of heparanase mRNA in bovine placenta during gestation.";
RL Reproduction 121:573-580(2001).
DR EMBL; AF281160; AAF87301.2;
DR InterPro: IPR005199; Glyco_hydro_79N.
DR Pfam: PF03662; Glyco_hydro_79N; I.
SQ SEQUENCE 545 AA; 61076 MW; FAC4BDFPD855B933 CRC64;

Query Match 80.4%; Score 2285; DB 2; Length 545;
Best Local Similarity 80.0%; Pred. No. 2, 2e-164;
Matches 436; Conservative 34; Mismatches 73; Indels 2; Gaps 1;

QY 1 MLIRSPALPPLMLL-LIGPLSPGALPPPAQADVDLDFTOEPLHVSFPLS 58
DB 1 MACRKPGRPLPLLLPLGLPSPGPGPAAAPADDAELEFTEPLHVSAPFAS 60
QY 59 VITDAWLADPRPLILIGSPKLTARGLSPAYLRFGTDTPLIDPKKESFEERSW 118
DB 61 FTIDAWLADPRFTFTLVSSKRTLARGLAPALRGNGGDLPLDPKKEPFEERSW 120
QY 119 QSQVNODICKYSGIPPDVEKRLLEWYEOQLLREHYOKKFNSTYSSSVDLTFAN 178
DB 121 LQSNODICKSGSPSDVEKRLLEWYEQVLLREQYOKKFNSTYSSSVMLTFAS 180
QY 179 CSGLDLIFGLNALRLPADLQWSSNAQLLDYCSSKGVNLSWELGNEPNSFLKADI 238
DB 181 CSGLNIFGVNALRLFTDMHSSNAQLLDYCSSKGVNLSWELGNEPNSFLKADI 240
QY 239 GSGLDGDFLOHMLRKSTFKAKLGVDPGPRRTAKMLKSLAAGGVDSVTHNY 298
DB 241 GRLGSDPFLKRLGSAFKAKLYGPDIGOPRRNTVKKLSFLAAGGVDSVTHNY 300
QY 299 YLNGRATREDPLNPDLIFISSVQKVPQVVESTRPGKKVMGETSSAYAGGAPLSDT 358
DB 301 YVNGRATREDPLNPDLIDFIFISSVQKTLRIVEKIRPKKVMGETSSAYAGGAPLSDT 360
QY 359 FAAGFMWLDKLGASNGIEVVMROVFFGAGNYHVDENFDPLDYWLSLFFKLVGTXY 418
DB 361 FAAGFMWLDKLGASNGIEVVMROVFFGAGNYHVDENFDPLDYWLSLFFKLVGTXY 420
QY 419 LMASVQSGSRKRLRYLHCTNTNPRYKSGEDLTLYALNHNVMKYLRLPFPNKQVDXY 478
DB 421 LMASVQSGSRKRLRYLHCTNTNPRYKSGEDLTLYALNHNVMKYLRLPFPNKQVDXY 480
QY 479 LRLPLPHGLKSVQNLGLTLKAVDDQTLPLIMKXPLRGSSSLGPAFYSFVIRNAK 538
DB 481 LRLPSGDLGLSVQNLGLTLKAVDDQTLPLIMKXPLRGSSSLGPAFYSFVIRNAK 540
QY 539 VAACT 543
DB 541 VAACT 545

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AC 08K3K3;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Heparanase (Mus musculus 0 day neonate thymus cDNA, RIKEN full-length
DE enriched library, clone:A43010LM04 product:heparanase, full insert
DE sequence).
GN Name=Hpa; Synonyms=Hpa, Hspe;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OC NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=FVB;
RA Miao H.-O., Navarro E., Patel S., Sargent D., Koo H., Wan H.,
RA Plata A., Zhou Q., Ludwig D., Bohlen P., Kusie P.;
RT "Cloning, expression, and purification of mouse heparanase.";
RL Protein Expr. Purif. 0:0-0(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Thymus;
RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning.";
RL Meth. Enzymol. 303:19-44(1999).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Thymus;
RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA RIKEN FANTOM Consortium;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Thymus;
RA The FANTOM Consortium;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
RN [5]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Thymus;
RX MEDLINE=2049374; PubMed=11042159; DOI=10.1101/gr.145100;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Kono H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subcloning of cap-trapper-selected cDNAs to
RT prepare full-length cDNA libraries for rapid discovery of new genes.";
RL Genome Res. 10:1617-1630(2000).
RN [6]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Thymus;
RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA Kono H., Akiyama J., Nishi K., Kitsuai T., Tashiro H., Itoh M.,
RA Sami N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwara S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA Onoe Y., Ishikawa T., Ozawa K., Tanaka T., Matsuda S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format
RT sequencing pipeline with 384 multicapillary sequencer.";
RL Genome Res. 10:1757-1771(2000).
RN [7]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Thymus;
RA Adachi U., Aizawa K., Akimura T., Hara A., Hashizume W.,
RA Fukuda S., Furuta M., Hanagaki T., Hara A., Hashizume W.,
RA Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hironaka T.,
RA Horii F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
RA Katoh H., Kawai J., Kojima Y., Kondo S., Kono H., Koda M., Koya S.,
RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,

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RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywinski M.I., Skalska U., Smalhus D.E., Scherch A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 RP SEQUENCE FROM N.A.
 RC TISSUE=Pancreas;
 RA Strausberg R.;
 RL Submitted (Apr-2003) to the EMBL/GenBank/DBJ databases.
 RN [6]
 RP SEQUENCE FROM N.A.
 RA Vlodavsky I., Friedman Y., Elkin M., Aingorn H., Atzmon R.,
 RA Ishai-Michaeli R., Bitan M., Pappo O., Perez T., Michal I.,
 RA Spector L., Pecker I.;
 RL Submitted (Apr-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF165154; AAD45379.1; -;
 DR EMBL; AF152376; AAD45669.1; -;
 DR EMBL; AF155510; AAD54941.1; -;
 DR EMBL; BC051321; AAH51321.1; -;
 DR EMBL; AF144325; AAD41342.1; -;
 DR GO; GO:0004566; F-beta-glucuronidase activity; TAS.
 DR GO; GO:0006029; P-proteoglycan metabolism; TAS.
 DR InterPro; IPR005199; Glyco_hydro_79N.
 DR Pfam; PF03662; Glyco_hydro_79n; 1.
 DR CHAIN 158 543 heparanase.
 SQ SEQUENCE 543 AA; 61176 MW; AD262EC267334AB2 CRC64;

Query Match 100.0%; Score 2841; DB 2; Length 543;
 Best Local Similarity 100.0%; Pred. No. 1.6e-206;
 Matches 543; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLRRKPPALPPMLLLGLPLSPGALPRPAQADVDLDFPTOEPLHLVSPFLST 60
 DB 1 MLRRKPPALPPMLLLGLPLSPGALPRPAQADVDLDFPTOEPLHLVSPFLST 60
 QY 61 IDANLATDPRFILLGSPKRLTARGLSPAYLRFGGTKTDFLIIDPKKESTFEERSYMOS 120
 DB 61 IDANLATDPRFILLGSPKRLTARGLSPAYLRFGGTKTDFLIIDPKKESTFEERSYMOS 120
 QY 121 QVNVODICKYGSIPPDVEEKLRLMPYQEOQLLREHYQKKFKNSTYSSSDVLYTFPANC 180
 DB 121 QVNVODICKYGSIPPDVEEKLRLMPYQEOQLLREHYQKKFKNSTYSSSDVLYTFPANC 180
 QY 181 GIDLIFGLNALRLTADLQWSSNAQLLDYCSSKGYNISWELGNEPNSFLKADIFIN 240
 DB 181 GIDLIFGLNALRLTADLQWSSNAQLLDYCSSKGYNISWELGNEPNSFLKADIFIN 240
 QY 241 QLGEDFIQLHKLRLKSTFNKAKLYGPDVGQPRRTAKMLKSLKAGGEVIDSVTMHHY 300
 DB 241 QLGEDFIQLHKLRLKSTFNKAKLYGPDVGQPRRTAKMLKSLKAGGEVIDSVTMHHY 300
 QY 301 NGRTATREDPLNDVDLDFISSVQKVFQYVESRPGKRWLGSTSSAYGGAPLLSDTFA 360
 DB 301 NGRTATREDPLNDVDLDFISSVQKVFQYVESRPGKRWLGSTSSAYGGAPLLSDTFA 360
 QY 361 AGFMMLDKLGLSARMGIEVVMROVFFGAGNYHLVDENFDPPLPYWLSLFLKLVGT 420
 DB 361 AGFMMLDKLGLSARMGIEVVMROVFFGAGNYHLVDENFDPPLPYWLSLFLKLVGT 420
 QY 421 ASVQSGSKRRKRLRYVLAHCTNTDNRKYEGDLTLAYALNHVTYKRLPYPPSNKOVDKY 480
 DB 421 ASVQSGSKRRKRLRYVLAHCTNTDNRKYEGDLTLAYALNHVTYKRLPYPPSNKOVDKY 480
 QY 481 RPLGPHGLLSKSVQNLGLTLKAVDDQTLPLMEKPLRPGSSLGLPASYSFFVIRNAKVA 540
 DB 481 RPLGPHGLLSKSVQNLGLTLKAVDDQTLPLMEKPLRPGSSLGLPASYSFFVIRNAKVA 540
 QY 541 ACT 543
 DB 541 ACT 543

RESULT 2
 ID 09UJ39 PRELIMINARY; PRT; 545 AA.
 AC 09UJ39, 01-MAY-2000 (TREMBlrel. 13, Created)
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
 DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
 DE Heparanase.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCB1_Taxid=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Placenta;
 RX MEDLINE=20229546; PubMed=10764835; DOI=10.1093/glycob/10.5.467;
 RA Dempsey L.A., Plummer T.B., Coombes S.L., Platt J.L.;
 RT "Heparanase expression in invasive trophoblasts and acute vascular
 RT damage.";
 RL Glycobiology 10:467-475 (2000).
 DR EMBL; AF084467; AAD54516.1; -;
 DR Genew; HGNC:5164; HSEB.
 DR InterPro; IPR005199; Glyco_hydro_79N.
 DR Pfam; PF03662; Glyco_hydro_79n; 1.
 SQ SEQUENCE 545 AA; 61417 MW; 67B80ACD73C5A9A1 CRC64;

Query Match 99.3%; Score 2820; DB 2; Length 545;
 Best Local Similarity 99.6%; Pred. No. 6.3e-205;
 Matches 543; Conservative 0; Mismatches 0; Indels 2; Gaps 2;

QY 1 MLRRKPPALPPMLLLGLPLSPGALPRPAQADVDLDFPTOEPLHLVSPFLST 58
 DB 1 MLRRKPPALPPMLLLGLPLSPGALPRPAQADVDLDFPTOEPLHLVSPFLST 60
 QY 59 VTIDANLATDPRFILLGSPKRLTARGLSPAYLRFGGTKTDFLIIDPKKESTFEERSYM 118
 DB 61 VTIDANLATDPRFILLGSPKRLTARGLSPAYLRFGGTKTDFLIIDPKKESTFEERSYM 120
 QY 119 OSQVNVODICKYGSIPPDVEEKLRLMPYQEOQLLREHYQKKFKNSTYSSSDVLYTFPAN 178
 DB 121 OSQVNVODICKYGSIPPDVEEKLRLMPYQEOQLLREHYQKKFKNSTYSSSDVLYTFPAN 180
 QY 179 CSGDLIFGLNALRLTADLQWSSNAQLLDYCSSKGYNISWELGNEPNSFLKADIFIN 238
 DB 181 CSGDLIFGLNALRLTADLQWSSNAQLLDYCSSKGYNISWELGNEPNSFLKADIFIN 240
 QY 239 GSQLGEDFIQLHKLRLKSTFNKAKLYGPDVGQPRRTAKMLKSLKAGGEVIDSVTMHHY 298
 DB 241 GSQLGEDFIQLHKLRLKSTFNKAKLYGPDVGQPRRTAKMLKSLKAGGEVIDSVTMHHY 300
 QY 299 YINGRTATREDPLNDVDLDFISSVQKVFQYVESRPGKRWLGSTSSAYGGAPLLSDT 358
 DB 301 YINGRTATREDPLNDVDLDFISSVQKVFQYVESRPGKRWLGSTSSAYGGAPLLSDT 360
 QY 359 FAAGFMMLDKLGLSARMGIEVVMROVFFGAGNYHLVDENFDPPLPYWLSLFLKLVGT 418
 DB 361 FAAGFMMLDKLGLSARMGIEVVMROVFFGAGNYHLVDENFDPPLPYWLSLFLKLVGT 420
 QY 419 LMASVQSGSKRRKRLRYVLAHCTNTDNRKYEGDLTLAYALNHVTYKRLPYPPSNKOVDKY 478
 DB 421 LMASVQSGSKRRKRLRYVLAHCTNTDNRKYEGDLTLAYALNHVTYKRLPYPPSNKOVDKY 480
 QY 479 LIRPLGPHGLLSKSVQNLGLTLKAVDDQTLPLMEKPLRPGSSLGLPASYSFFVIRNAK 538
 DB 481 LIRPLGPHGLLSKSVQNLGLTLKAVDDQTLPLMEKPLRPGSSLGLPASYSFFVIRNAK 540
 QY 539 VACT 543
 DB 541 VACT 543

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 23, 2005, 11:18:07 ; Search time 109.5 Seconds
(without alignments)
2539.352 Million cell updates/sec

Title: SEQ2B
Perfect score: 2841
Sequence: 1 MLNRKSPALPPEMLDLGP.....LPASFSFVJINNAKVAACI 543

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues
Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_03:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2841	100.0	543	2	Q9Y251 homo sapien
2	2820	99.3	545	2	Q9UL39
3	2285	80.4	545	2	Q9MYX0
4	2153	75.8	535	2	Q8K3K3 mus tauris
5	2143	75.4	535	2	Q6Y6Z1 mus musculu
6	2138	75.3	536	2	Q711P1 rattus norv
7	2126	74.8	536	2	Q9Q2F8
8	1648.5	58.0	523	2	Q9QXK5
9	1150.5	40.5	592	2	Q9HB37
10	1142.5	40.2	592	2	Q8WMQ2
11	1011.5	35.6	548	2	Q8WMQ1
12	932.5	32.8	534	2	Q9HB38
13	893.5	31.5	480	2	Q9HB39
14	699	24.6	515	2	Q8T108
15	417	14.7	521	2	Q9SDA1
16	417	14.7	543	2	Q9FPI0
17	400	14.1	559	2	Q89F99
18	392.5	13.8	544	2	Q8H515
19	379	13.3	541	2	Q69116
20	365	12.8	527	2	Q9LRC8
21	365	12.8	537	2	Q70VJ3
22	363	12.8	536	2	Q9FZP1
23	353.5	12.4	516	2	Q9FUK6
24	353.5	12.4	539	2	Q8L608
25	350.5	12.3	529	2	Q6ZUE2
26	169.5	6.0	190	2	Q82604
27	156	5.5	935	2	Q9VE79
28	141	5.0	559	2	Q7SRB0
29	138.5	4.9	463	2	Q63T97
30	126.5	4.5	493	2	Q9HK01
31	118.5	4.2	408	2	Q9HEZ1

32	118.5	4.2	408	2	Q9HEZ2	Q9he22 phanerochae
33	116.5	4.1	617	2	Q40996	Q40996 measles vir
34	116	4.1	390	2	Q8TPH7	Q8TPH7 methanosarc
35	114.5	4.0	1169	2	Q869K5	Q869K5 dictyostell
36	114	4.0	398	2	Q72RP7	Q72RP7 leptospira
37	114	4.0	398	2	Q8F410	Q8F410 leptospira
38	113.5	4.0	617	2	Q8J295	Q8J295 measles vir
39	113.5	4.0	1829	2	Q9KH44	Q9KH44 pantoea agg
40	112.5	4.0	617	2	Q83647	Q83647 measles vir
41	112	3.9	732	2	Q7MSD4	Q7msd4 wolinnella s
42	112	3.9	2319	2	Q96U00	Q96U00 neurospora
43	111.5	3.9	617	2	Q40991	Q40991 measles vir
44	111.5	3.9	617	2	Q98VH5	Q98VH5 measles vir
45	111	3.9	670	2	Q9M090	Q9M090 arabidopsis

ALIGNMENTS

RESULT 1	ID	Q9Y251	PRELIMINARY;	PRT;	543 AA.
AC	Q9Y251;				
DT	01-NOV-1999	(TEMBLrel. 12, Created)			
DT	01-NOV-1999	(TEMBLrel. 12, Last sequence update)			
DT	25-OCT-2004	(TEMBLrel. 28, Last annotation update)			
DE	Heparanase.				
GN	Name=HPA; Synonyms=HPSE;				
OS	Homo sapiens (Human)				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.				
OX	NCBI_TaxID=9606;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	TISSUE=Placenta;				
RX	MEDLINE=99321245; PubMed=10395326;				
RA	Hulett M.D., Freeman C., Handorf B.J., Baker R.T., Harris M.J.,				
RA	Parish C.R.;				
RT	"Cloning of mammalian heparanase, an important enzyme in tumor				
RT	invasion and metastasis."				
RL	Nat. Med. 5:803-809(1999).				
RN	[2]				
RP	SEQUENCE FROM N.A.				
RC	TISSUE=Placenta;				
RX	MEDLINE=99335379; PubMed=10405343; DOI=10.1006/dbrc.1999.0962;				
RA	Kusie P.H., Holmes J.D., Ludwig D.L., Patel S., Navarro E.C.,				
RA	Seddon A.P., Giorgio N.A., Bohlen P.;				
RT	"Cloning and functional expression of a human heparanase gene;"				
RL	Biochem. Biophys. Res. Commun. 261:183-187(1999).				
RN	[3]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=99377052; PubMed=10446189; DOI=10.1074/jbc.274.34.24153;				
RA	Toyoshima M., Nakajima M.;				
RT	"Human heparanase. Purification, characterization, cloning, and				
RT	expression."				
RL	J. Biol. Chem. 274:24153-24160(1999).				
RN	[4]				
RP	SEQUENCE FROM N.A.				
RC	TISSUE=Pancreas;				
RX	MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;				
RA	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,				
RA	Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schaller G.D.,				
RA	Altshul S.F., Zeeberg B., Buettow K.H., Schaefer C.F., Bhat N.K.,				
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,				
RA	Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,				
RA	Stapleton M., Soares M.B., Bonaldo W.F., Caesavari T.L., Scheetz T.E.,				
RA	Brownstein M.J., Udell T.B., Toshiyuki S., Carninci P., Pange C.,				
RA	Raha S.S., Loquellano N.A., Peters G.J., Abrazon R.D., Mullany S.J.,				
RA	Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,				
RA	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,				
RA	Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,				
RA	Fahney J., Helton E., Ketterman M., Madan A., Rodrigues S., Sanchez A.,				
RA	Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,				

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A:Gene: ADE1; SPDB:SPBC405.01
A:Map position: 2
C:Superfamily: Saccharomyces cerevisiae ADE5 multifunctional protein; phosphoribosylamir
C:Keywords: cyclo-ligase; putine nucleotide biosynthesis
F/5-425/Domain: phosphoribosylamine-glycine ligase homology <PGL>
F/439-767/Domain: phosphoribosylformylglycinamide cyclo-ligase homology <PFL>

Query Match 3.7%; Score 104.5; DB 1; Length 788;
Best Local Similarity 27.7%; Pred. No. 15;
Matches 70; Conservative 36; Mismatches 114; Indels 33; Gaps 11;

QY 297 HYLNGRTATRE--DELNDV--LDIFISSVQKVFQVVEST--RPGKKWLGETSSAY---- 348
DB 424 HHALNPKRKTRREILTYENGSGVNDNGNEFQRIKDLVSTRPADADIGCGJFDLQ 483
QY 349 -GGAPL--SDTPAAGFMULDKGLSAR--MGIEVVMRQVFGAGNYHLVDENPDL--P 402
DB 484 AGMNDPLVASATDGVGSKLLIALSLNKHDTVGIDVAMNV-----NDLVQGAEPILFL 537
QY 403 DYMILSLFKKLVGTKVLAMSVQSGKRRKLRVYLHCTNTDNPRYKEGDLTLVAINLHNTK 462
DB 538 DIFATGSLDLKYSTSVGEVQCKQAGALVGETSEMPGLYHGHYDANGTSVAVSR 597
QY 463 YRLPYPFSSNKQVDKYLRLPLGPHGLSKSVQDLNGLTL--KMVD---DQTLPLMEKPL 516
DB 598 DDLPRKESFSGKDILL-----GLASGVHNSNGYSLVRKIYVESDLEYTSVCPMDKNV 650
QY 517 RRGSSSLGPAFSY 529
DB 651 RLGDSTLILPTRIY 663

RESULT 15

F70411

adenylosuccinate synthetase - Aquifex aeolicus

C:Species: Aquifex aeolicus

C:Date: 08-May-1998 #sequence_revision 08-May-1998 #text_change 09-Jul-2004

C:Accession: F70411

R.Deckert, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.E.; Oy

V. Nature 392, 353-358, 1998

A:Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus.

A:Reference number: A70300; MUID:98196666; PMID:9537320

A:Accession: F70411

A:Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Residues: 1-432 <AOF>

A:Cross-references: UNIPROT:O67321; GB:AB000733; NID:92983720; PIDN:AA07286.1; PID:9298

A:Experimental source: strain VFS

C:Genetics:

A:Gene: purA

C:Superfamily: adenylosuccinate synthase

Query Match 3.7%; Score 104; DB 2; Length 432;
Best Local Similarity 23.9%; Pred. No. 6.4;

Matches 96; Conservative 39; Mismatches 128; Indels 138; Gaps 22;

QY 15 LLLGLPLGPLSPALRRPAQADVLD-----FTQEPHLVSPS 55
DB 51 IALLPTGLIHEHVKGIVAGM--VVDLEVLHKEVKNLEEKIYKERLFTSDRAHLWMPY 109
QY 56 FLSTVIDANLATPRLIILGSPK--LRTIARGISPAVL-RFGGKTDFLIPDKKESTP 112
DB 110 H-----KLLDSLFEKKKGIGTLRGIGRAYMFKY--RKGIKISDLKDEKRF 154
QY 113 EERSYWGQVQVODICKYGIIPDVEEK-----LRLWPYQQLIREHYQKKFKNSTY 165
DB 155 ----YTLLEBNLDVFK-----NICEKVCEKFDLDINOIYEOL-----RYFEFEKENV- 199
QY 166 SRSSVDVLYTFANCSGLDLIFGLNALRLTADL-----QMSNSNAQLLDYCSSKGVNISWE 221
DB 200 ----VDLLRPFNTQKGSVLFEGAGQTLTLDVDMGTYPYVTSNASAL-----GLSNG 246

QY 222 LGNEBNSFLKKADIFING-----SOL-GEYIQLHKLRLKSTFKQAKLYG 265
DB 247 TGMPPKVF---SDAPFLGVAKAYTTRVGBGPFPTLKGEBEGEKRL------GGEYG 295
QY 266 PVVGQPRR---KTAKMLKSLKAGGEVIDSVTHHHYILNGRTATREDPLN------ 313
DB 296 STTGRRRCGMWLDVALKRYAVQVNG-----LDGFVITKLDVLDITPDEVKVCVA 343
QY 314 -----VDLDIFISSVQKVFQV--VESTPRGKKWLGETSSA 347
DB 344 YELDGEVIDYFPASYSBELRWKPFYKTLKG---WKKSTKGA 381

Search completed: March 23, 2005, 11:31:39
Job time : 30 secs


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QY 164 TYSRSSVDVLYTFANCSGDLIFGL-NALLRTADLQMNSSN-----AQLLDYC----- 211
D 121 -----GIDIK-----ADLSGALVLSLPOALEYDTINMDPPSRWDGISGLDIADYSITAO 182
QY 212 -----SSKGVNI-GMEL-GNEPNSFL--KKADIFINSQ----- 241
D 183 RHEENGDDSDNEISGNGTVGNLGAARLRADMDQDTYLSKSNDDVDVINGDPTQKWEWSR 242
QY 242 -----LGEDYIQLHKLLRKSTF-----KNAKLYGPDV 268
D 243 YYAMRALPELKAAGIGEDY-----LNSDIFDGNFYVGSISTDQMLPRLRGAPDI 296
QY 269 GQPRKRTAMKLSFLKAGEVI-----DSVTWHYILNGRTATREDFLN 312
D 297 SGVAHTTAKVTVSOL--GRVYETQVPAGPPIODLGDSV-----SGTLHIREON 346
QY 313 PVLVDIFISSVQKVPQVSTRPKG--KVWL-----GENTS----- 345
D 347 GGVQEDINTASMPF---LTRPGQVRKLMGGRPOEWHVHGEGFSGEASWGIANCW 402
QY 346 SAYGGAPPLSD-----TPAA-----GFWMLDKL-----GLSAR 374
D 403 SLYGA--LADENHQSALGVRDLSTVGAVAFDTHSHRTLDKETAYGKSLDGNFR 459
QY 375 MGI-----EVNMRQVFEAGNTHLVDENFDPDPLDYWLSLFFKLYGT--KVLMAVQGS 426
D 460 LSYSKDFEILNRSRVFAG--YRFESENMVTSEY-LDASDEEMVATGNDKEMVATATVNO 515
QY 427 KRRKRVYHCTNTNPRKEDDLTYAL-----NLHNVTK----- 462
D 516 NERDAGVSAYLVYTRTYVDRDEQTYNWLSHYFGLSIRNMSSIMTGYRYEYDQADK 575
QY 463 --YLRLPYPSNKKQVDKYLRLPLGPHGLSKSVQLNGLTFLKVVDPOT 507
D 576 GYIISLSPWGDSSSTISY-----NGNVGSGSDSSQVQ--YFSKVDAT 616

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RESULT 10
S74760
Hypothetical protein sir1617 - Synechocystis sp. (strain PCC 6803)
C:Species: Synechocystis sp.
A:Variety: PCC 6803
C:Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004
C:Accession: S74760
R:Kaneko, T., Sato, S.; Kocani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.;
O. K.; Okumura, S.; Shimo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda
DNA Res. 3, 109-136, 1996
A:Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis
S.
A:Reference number: S74322; MUID:97061201; PMID:8905231
A:Accession: S74760
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-411 <KAN>
A:Cross-references: UNIPROT:P72895; EMBL:D90901; GB:AB001339; NID:G1651897; PIDN:BA1691
A>Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996

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Query Match 3.8%; Score 108.5; DB 2; Length 411;
Best Local Similarity 21.4%; Pred. No. 2.7; Mismatches 94; Indels 93; Gaps 17;
Matches 66; Conservative 55;
159 KFNSTYSRSSVDVLYTFANCSGDLIF--GMLALRTADLQMNSSNAQL----- 206
D 151 EFRLLSPTRQIDID--FAGSTKLDLLASBENIDCVHLANPRVYTSNVAMQDTLMLAN 207
QY 207 LLDYCSSKG---YNI SMEL-----GNEPNSFLK-----ADIFNSQDCE 244
D 208 VIDVCIACKIPIPIYPSWEIYSGVAGTIAHDESTPLAPRGYETKYLAELIL----- 260
QY 245 KYIQHLKLRKSFNKAUKYGPVQGRPKRTAKMLKSLKAGEVLDSTWHHYLYNGRT 304
D 261 DHCRRTRGLRCALRRSPVYGSMDKP-----KFTFNFRKASQGGKIVT--HHYING-- 311

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QY 305 ATREDFLAPDV---LDIFISSVQKVPQVSTRPKGKVMIGETSSAYGGAPLSDPFA 360
D 312 -----NPKDLHLHIDILSISVATL-----KSRFINLNI-----GTGQLSSTLK 351
QY 361 AGFWMLDKLGLSA-----RMGIEVVMRQVFPAGNTHLVDENFDPDPLDYWLSLFFKLYG 415
D 352 IAEKTRDELGSSSMIQIETVNTFVASIANVYGRAN-HVLD-----WEVYIFE-QG 400
QY 416 TKVLMASV 423
D 401 LKSLHQI 408

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RESULT 11
D87541
beta-xylosidase [imported] - Caulobacter crescentus
C:Species: Caulobacter crescentus
C:Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Jul-2004
C:Accession: D87541
R:Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.I.
B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolton
n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.
Proc. Natl. Acad. Sci. U S A. 98, 4136-4141, 2001
A:Title: Complete Genome Sequence of Caulobacter crescentus.
A:Reference number: A87249; MUID:21173698; PMID:11258647
A:Accession: D87541
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-500 <STO>
A:Cross-references: UNIPROT:Q9A5U0; GB:AE005673; NID:G13423886; PIDN:AAK24328.1; GSPDB:IG
A:Gene: CC2357

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Query Match 3.8%; Score 107.5; DB 2; Length 500;
Best Local Similarity 25.7%; Pred. No. 4.4; Mismatches 80; Indels 47; Gaps 15;
Matches 56; Conservative 35;
165 YSRSSVDVLYTFANCSGDLIFGLN--ALLRTAD--LQW--NSSNAQL-----LLD-- 209
D 81 YDMTKIDQLYDALLAKGIFELGFTPRAMKTSQDTFYWMGNTHSPKLGPRDLIDAF 140
QY 210 -YCSSKGVNI---SW--ELGNEPN--SFLKADDFINSQGEYIQLHKLLRKSTFKN 260
D 141 VHLRLARVGVEERKTFWFVWNEPNLDGWEVAD-----QAAVFEIYDV--TARA 188
QY 261 AKLYGPD--VQPRKRTAKMLKSLF--KAGEVIDSVTHHYLYNG--RTATREDPL 311
D 189 IAIIDPSLRVSGPATRGAAMVPEFLAHYKSSAAYDFYTHRYGVGDGFLDKRGVDTKL 248
QY 312 NPVDLDIFISSVQKVPQVFE--STRPGKVMIGETSSAY 348
D 249 SPSD-DAVVGDVRRVREGIEASAPGLPLFYFTEMSTSY 285

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RESULT 12
F85875
probable fimbrial usher Z3600 [imported] - Escherichia coli (strain O157:H7, substrain EI
C:Species: Escherichia coli
C:Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004
C:Accession: F85875
R:Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glaesner, J.D.; Rose, D.J.; Mayhew,
iller, L.; Grotbeck, E.J.; Davis, N.W.; Lam, A.; Dimatata, E.; Potamoustis, K.; Apodaca,
Nature 409, 529-533, 2001
A:Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A:Reference number: AB5480; MUID:21074935; PMID:11206551
A:Accession: F85875
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-879 <STO>
A:Cross-references: UNIPROT:Q8XCP4; GB:AE005174; NID:G12516702; PIDN:AA657466.1; GSPDB:GT
A:Experimental source: strain O157:H7, substrain EDJ933
C:Genetic:
A:Gene: Z3600

```


Db 14 IRKMKIYNGKNEKDIKERLIKE-----LKEHVLVETEDGTYYTLKADEENMSKV 66
 QY 172 -----VLTPFANCSGLDIFGLNALLRTADLQWSSNQMLLDYSSSKGYNISWEIGNEP 226
 Db 67 GALKKAIYKFAKPS-----KITDL-----SNPR-VLDLCSGNGYNAIALLHYNK 109
 QY 227 NS-----FL-----KKADIFINGSQLEGDYIQLHKLKRSKF 258
 Db 110 NAEIMWEICEEVLFLTLFLDIPIYKHEHETIKDKVREYFLN--KIGLEY-----KSDY 159
 QY 259 KNAKIYGPVGVOPRRKRTAAMKLSFLKAGEVIDSTWTHYYLNGRTAT--REDFLNPDVL 316
 Db 160 DNINLY--VGPARKFIIKSDKKY-----NVFHDAPSPKDPITYTYDFL----- 202
 QY 317 DIFISSVOKFQOVNSTRPGKVMYIGETSSAYGGAPLSDTFPAGFMWLDKLGASRWG 376
 Db 203 -----KEIYKRMEDN--GVLI-----SYSSAIPFSSALVDGCFVISEKESVGRKRG 246
 QY 377 IEVNRQVFFGAGNYHLDENFD-----PLPDYMLSLFKKVLGTVKVLMAVSGSKRR 429
 Db 247 ILLAVKNPWFKNRINEVDERVALSVIALPYRDETLSTKDKITIEDREERKLEKLI 306
 QY 430 KIRVYLHCNTNTPRYKEDDLTYA--INLHANTYKLRUPY 468
 Db 307 KIGKYLSTQIKKNIPEELIKIOKEDLNSSEIIKMKRLKF 347

RESULT 5

T12094
 beta-fructofuranosidase (EC 3.2.1.26) - fava bean
 C:Species: Vicia faba (fava bean)
 C:Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004
 C:Accession: T12094
 R:Weber, H.; Borisjuk, L.; Heim, U.; Buchner, P.; Wobus, U.
 Plant Cell 7, 1835-1846, 1995
 A:Title: Seed coat-associated invertases of Fava bean control both unloading and storage
 A:Reference number: Z17416; MUID:96093423; PMID:8535137
 A:Accession: T12094
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-575 <WEB>
 A:Cross-References: UNIPROT:Q43855; EMBL:Z51562; NID:g861154; PIDN:CAA84526.1; PID:g8611
 A:Experimental source: cv. F110, seed coat
 C:Genetics:
 A:Gene: CMINV1
 C:Superfamily: beta-fructofuranosidase
 C:Keywords: cell wall; glycoprotein; glycosidase; hydrolase

Query Match 3.9%; Score 111.5; DB 2; Length 575;
 Best Local Similarity 21.4%; Pred. No. 2.7;
 Matches 72; Conservative 48; Mismatches 107; Indels 109; Gaps 19;

QY 46 QEPPLHVS-----PSFLSYTIDANLADPRFLILGSPKRTLARGLS-----P 89
 Db 228 KPHISAKRTGMWECDFPVSLGKNGLD--LSMMGNVXHVKNLSIDITREYETTG 285
 QY 90 AYLR-----FGTKTDF-----LIPPKKESTPEERSYW-----OSOVNQ 124
 Db 286 TYLQNDQDKTIPDKTSMDGGLRYDGNFYASKSPFDPK-----NRRIIWGANESDTE 341
 QY 125 DICKYG-----SIPDV-----EEKLLEWYOEOILLR-----EHYOKKFNSTYSRSSV 170
 Db 342 DQVKGMAGIQAIPTVWLDSRRQLR--QMPVEELRLRGQVEMKRLKKGGY-----L 396
 QY 171 DVLVTFPANGSGDLIFGLNALLRTADLQWSSNAQMLLDYSSSKGYNISWEIGNEP 230
 Db 397 EVKGITASQADVETFSISLXAEAFDPNWEVAE--DLCAQSGSKVGVG--PFGILL 451
 QY 231 KKADIFINGSQLEGDYIOL-----HKLL-----RKSTFNKATLYGP-----DV 268
 Db 452 TILA-----SKLEBETTSVFFRVFRKANGHKILMCDASSSSLNRELYRPSAGFVNVDL 505
 QY 269 GQPRKRTAAMKLSFLKAGEVIDSTWTHYYLNGRT 304

Db 506 GNNKKLSLRSLL-----IDHSVESFVGSGKT 531

RESULT 6

T10666
 hypothetical protein F6E21.40 - Arabidopsis thaliana
 C:Species: Arabidopsis thaliana (mouse-ear cress)
 C:Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004
 C:Accession: T10666
 R:Bevan, M.; Lennard, N.; Quail, M.; Harris, B.; Rajandream, M.A.; Barrell, B.G.; Bancroft
 submitted to the Protein Sequence Database, June 1999
 A:Reference number: Z16533
 A:Accession: T10666
 A:Molecule type: DNA
 A:Residues: 1-670 <BEV>
 A:Cross-References: UNIPROT:Q9M090; EMBL:AL049914; GSPDB:GN00062; ATSP:F6E21.40
 A:Experimental source: cultivar Columbia; BAC clone F6E21
 C:Genetics:
 A:Gene: ATSP:F6E21.40
 A:Map position: 4
 A:Introns: 47/3; 87/1; 123/3; 203/3; 230/2; 255/3; 284/3; 305/1; 335/3; 347/3; 370/3; 393;
 C:Superfamily: Schizosaccharomyces pombe negative regulator of mitosis ehb1

Query Match 3.9%; Score 111; DB 2; Length 670;
 Best Local Similarity 22.4%; Pred. No. 3.7;
 Matches 123; Conservative 77; Mismatches 194; Indels 156; Gaps 33;

QY 51 LVSPSFLSTIDANLATDPRFLILGSPKRTLARGLSPAY--LRFSGTKTDFLIFDPK- 107
 Db 47 LVDPSYRBSLVNBN--GVDTQVLPVCGSDLV-----LSPQWSSHVGVKISSWIDLSD 99
 QY 108 -----KESTPEERSYWQOVNQDICKYSSIPDVEEKLRLWEPYOELLREHYOKKER 161
 Db 100 EYLRMSDETTLKQELAMATHLSIQWCE-----PD-----LTPHYLAGGL 139
 QY 162 NSTYRSSV---DVLV-----TPANCS--GLDILFGLNALLRTADLQWSSNAQML 207
 Db 140 RVSCCRSSEFISDETLKYTFNQALTFGSSSLFCINVISALMLWRLVPLV--SEGDGM 196
 QY 208 LDYSSKGYNISWEIGN-----EENSFLKA--DIFIN-----GSQLEGDYIQLHKL 253
 Db 197 DD--TSBGLDSWEIWNSEFRLLCEHDSKLSVALDVLTSLPSTSGRWGGS--VRAILS 253
 QY 254 RKSTFNKATLYGPDVGP--RRKTAAMKSLF--KAGEVIDSTWTHYYLNGRTATREDF 310
 Db 254 TDAFLTNAR-----GYPLSKRHQKLTAGFDHAQVVICRPVHNLQKPLDSSSECTE 307
 QY 311 INPDVLDIFISSVQKVPQVVESTPRGKVMYIGETSSAYGGAPLSDTFPAGFMWLDKLG 370
 Db 308 KNP--LRIYLDVVAALFQMBESLSEQRIETELGYRDFLQAPLQPLMDNLEAQTYETFE-- 362
 QY 371 LSARGLIEVWQVFFGAGNYHLDENFDPLPDYMLSLFKKVLGTVKVM----- 420
 Db 363 --RSVKTYOYO--RAVEKALVDR--VPDEKASEL-----TIVLMVVGAGRGPLY 406
 QY 421 -ASVQSKR--RKLRYVYLCTNTDNPRYKEGDLTYVAINLHNVTK-----YLRLEY 468
 Db 407 RASLQAABETDKKLVY--AVEKNPN-----AVYTLHLVLMKEGVEDVVTIISCOM 455
 QY 469 PPSN--KQVDYKTLRPLGHLGSLKSVQNLGTLKMWDDQTLPLM--EKLPRGSSISG 523
 Db 456 RFWNNAPEQADIIIVSEILGSGF-----DNELSPEDICDAQRLKP--DGIS 498
 QY 524 LPAFSYSPFV 533
 Db 499 IPS-SYTSFT 507

RESULT 7

S32961
 hypothetical protein YBR259w - yeast (Saccharomyces cerevisiae)
 N:Alternate names: hypothetical protein YBR1727

QY 411 KKLVTGKVLMAVSGSKRR-----KLRYLHCTNTDNPYKGGDLTLVAINLHNT 461
 DB 337 KRLIGKVLAVHVAIGQRPRGRVIRDLRIYAHCTNHNHNHYVAGSTLTFLINHRSR 396
 QY 462 KYRLPLPPSKNQVDKYLLPLPGPHGLSKSVQNLGTLKMDQDTLPPLMEKPLRPGSS 521
 DB 397 KKIKLAGTLRDLVHQLDLPYGOEGLSKSVQNLGTLKMDQDTLPPLMEKPLRPGRT 456
 QY 522 LGLPAFSYSPFYIRNAKVAAC 542
 DB 457 LVIPVYMGFVYKVNALAC 477

RESULT 2

T45608

hypothetical protein F13G24.30 - Arabidopsis thaliana

C/Species: Arabidopsis thaliana (mouse-ear cress)

C/Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 09-Jul-2004

C/Accession: T45608

R.Beaven, M.; Van Der Schueren, J.; Chuang, Y.U.; Voelt, M.; Robben, J.; Volckaert, G.; Be
 submitted to the Protein Sequence Database, December 1999

A/Reference number: Z23009

A/Accession: T45608

A/Status: preliminary

A.Molecule type: DNA

A.Residues: 1-521 <BEV>

A.Cross-references: UNIPROT:Q9SDA1; EMBL:AL133421

A.Experimental source: cultivar Columbia; BAC clone F13G24

C/Genetics:

A.Map position: 5

A.Introns: 53/3; 66/1; 127/2; 177/1; 256/1; 319/2; 361/2; 394/3

A.Note: F13G24.30

Query Match 14.6%; Score 416; DB 2; Length 521;
 Best Local Similarity 29.2%; Pred. No. 5.8e-23;

Matches 154; Conservative 68; Mismatches 184; Indels 122; Gaps 24;

QY 75 LGSPLKRLTARGLSPAYLRFSGTKTDFLFDPKKESTFEERSYVQGVNODICKYGSIP 134
 DB 55 LRRPLTKAIKAKFKPIRIGSLQDVLYDVGNLKT-----PCR----- 94
 QY 135 DVEEKLRLMPYQEOQLLREHYOKFKNS---TYSRSV-----DVLTYFANCSGLDLIF 186
 DB 95 -----PQOKM-----NGLGFGSKGLMKRMKMDLNSFLRTGAVTF 132
 QY 187 GINALILRTDLQ-----WNSNAQLLDYCSKGYNT-SNELGEPNSFLKADIFIN 238
 DB 133 GINALRGRHKLKRGKAWGAMDHINTDPLNTYVSKGYVIDSWEFGNELSG--SGVGASVS 190
 QY 239 GSQLEGDIYQLHKLKSTFKNAKLYGPPVGOP-----RRKTAKMUKSFLKGGEVYDSV 293
 DB 191 AEYKGLIYLVKDVINK-VYKSMHLKPIIVAPGCGYEQOWTKLEI---SGPSVADV 246
 QY 294 TWHHYLLNGRT--ATREDFLNPVDLDFISVQKVF---QVESSTRPKKWLGETSSA 347
 DB 247 THHIYVLGSGNDPALVKIIMDP-----YLSQVSKTFKDVNQTIGEHGPMASPVGSSGA 302
 QY 348 YGGGALISDTFPAAGMMIDKLGSLKRMGIEVMYQVFGAGNYHLVDR--NPEDLPDYKL 406
 DB 303 YNSGGHNVBDTFIDSFYWLIDQLMSNRHNTKYVCRQTLVG--GFYGLLEKTFPNDYYS 361
 QY 407 SLTFKLVTGKVLMAVSGSKRRKLVYLHCTNTDNPYKGGDLTLVAINLHNTKYL-- 464
 DB 362 ALLMHLKMGKVLAVOTDPP--QLRVYAHCSK-----GRACVTLILLNLSQSPFTYS 413
 QY 465 -----RLPYPS---NKQVDKYLIR--LGPHG--LISKSVQL 495
 DB 414 VNSGINVVLNAESRKKKSLDLTKRPFMSVIGSKASGYLNRBEYHLTPENGVLRSKTMVL 473
 QY 496 NGTLTKMVDQDTLPPLMEKPLR--GSSGLPFAFSYFFPIYIRNAKVAAC 542
 DB 474 NKSILKPTATGDIPL--EPVLSVNSPLNVLPLSMSTFVLPNFDASAC 520

RESULT 3

T01953

hypothetical protein T2L5.6 - Arabidopsis thaliana

C/Species: Arabidopsis thaliana (mouse-ear cress)

C/Date: 26-Feb-1999 #sequence_revision 26-Feb-1999 #text_change 09-Jul-2004

C/Accession: T01953

R.Giesel, C.; Smith, A.; Le, T.
 submitted to the EMBL Data Library, October 1998

A/Description: The sequence of A. thaliana T2L5.

A/Reference number: Z14470

A/Accession: T01953

A/Status: translated from GB/EMBL/DBJ

A.Molecule type: DNA

A.Residues: 1-190 <GEI>

A.Cross-references: UNIPROT:O82604; EMBL:AF096371; NID:g3695386; PID:g3695392

A.Experimental source: cultivar Columbia

C/Genetics:

A.Map position: 4

A.Introns: 36/2; 69/3

A.Note: T2L5.6

C/Superfamily: Arabidopsis thaliana hypothetical protein T2L5.6

Query Match 6.0%; Score 169.5; DB 2; Length 190;
 Best Local Similarity 27.8%; Pred. No. 2.5e-05;

Matches 54; Conservative 34; Mismatches 57; Indels 49; Gaps 9;

QY 382 ROVFPGAGNYHLVD--ENFDPLPDYLSLFFKLVTGKVLMAVSGSKRRKRLRYLHCTNT 440
 DB 12 RQSLIG-GNYGLNTNTFTPNPDYSAIWRQLMGRKALFTTFSQTK--KIRSYTHCA-- 66
 QY 441 DNPYKGGDLTLVAINLHNV-----TKYLRPLPPSKNQVDKYLLRPL 483
 DB 67 ---RQSKG-ITVLMNLDNTTIVAKVELANSFSLRHKKMK-----SKRASSQLFG-- 115
 QY 484 GPHGLL-----SKSVQNLGTLKMDQDTLPPLMEKPLRPGSSGLPAPS 528
 DB 116 GNGVYQREHYHLTAKDGLHSQTMNLGNALQVNSMGDLPIEPIHINSTEPIITAPYS 175
 QY 529 YSFPYIRNAKVAAC 542
 DB 176 IVFVHRNVVPAC 189

RESULT 4

F64383

hypothetical protein M0670 - Methanococcus jannaschii

C/Species: Methanococcus jannaschii

C/Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004

C/Accession: F64383

R.Bult, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blake, J.
 ; Reich, C.I.; Overbeek, R.; Kirkness, E.F.; Weissbrock, K.G.; Merrick, J.M.; Glodek, A.;
 Ison, J.D.; Sadow, P.W.; Hanna, M.C.; Cotton, M.D.; Robert, K.M.; Hurst, M.A.
 Science 273, 1058-1073, 1996

A/authors: Kaine, B.P.; Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; Woese, C.
 A./title: Complete genome sequence of the methanogenic archaeon, Methanococcus jannaschii.
 A./reference number: A64300; MUID:96337999; PMID:8688087

A/Accession: F64383

A/Status: preliminary

A.Molecule type: nucleic acid sequence not shown; translation not shown

A.Residues: 1-356 <BUL>

A.Cross-references: UNIPROT:Q58084; GB:U67514; GB:L77117; NID:g2826304; PIDV:AA89664.1;

C/Genetics:

A.Map position: REV596956-595886

A/start codon: GTG

Query Match 4.0%; Score 112.5; DB 2; Length 356;
 Best Local Similarity 21.2%; Pred. No. 1.1;

Matches 85; Conservative 48; Mismatches 143; Indels 125; Gaps 18;

QY 126 ICKY-----GSIPDVEKRLRMPYQEOQLLREHYOKFKKSTYSRSSVD----- 171



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OM protein - protein search, using sw model

Run on: March 23, 2005, 11:19:33 ; Search time 27 seconds
(without alignments)
1935.026 Million cell updates/sec

Title: SEQ2A
Perfect score: 2842
Sequence: 1 MLRSEKPLPPLMLLLGP.....LPAFSYPFVIRNAKVAACI 543

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	897.5	31.6	480	2 JC7506	heparanase protein
2	416	14.6	521	2 T45608	hypothetical prote
3	169.5	6.0	190	2 T01953	hypothetical prote
4	112.5	4.0	356	2 F64383	hypothetical prote
5	111.5	3.9	575	2 T12094	beta-fructofuranos
6	111	3.9	670	2 T10666	hypothetical prote
7	111	3.9	688	2 S32961	hypothetical prote
8	111	3.9	2298	2 T49648	hypothetical prote
9	109.5	3.9	879	2 E91031	probable outer mem
10	108.5	3.8	411	2 S74760	hypothetical prote
11	107.5	3.8	500	2 D87541	beta-xylosidase [1
12	106	3.7	879	2 F85875	probable fibrinoly
13	105	3.7	670	2 T38446	microtubule-associ
14	104.5	3.7	788	1 S00652	phosphoribosylamin
15	104	3.7	432	2 F70411	adenylosuccinate s
16	104	3.6	2013	2 A11489	probable peptidogl
17	103.5	3.6	587	2 S36231	beta-fructofuranos
18	103.5	3.6	676	2 AF1153	transcription anti
19	103.5	3.6	687	2 F85188	retrotransposon 11
20	103	3.6	796	2 D97065	transketolase (imp
21	101	3.6	594	2 A82913	hypothetical prote
22	101	3.6	644	2 A97268	methionyl-tRNA syn
23	100.5	3.5	805	2 H72098	DNA gyrase, chain
24	100.5	3.5	805	2 C86525	DNA gyrase subunit
25	100.5	3.5	510	2 AE2140	toxin secretion AB
26	99.5	3.5	510	2 H69883	conserved hypotet
27	99.5	3.5	837	1 A31842	endo-1,4-beta-xyla
28	99	3.5	897	2 G02529	dynein heavy chain
29	99	3.5	4644	1 A38905	dynein heavy chain

30	98.5	3.5	596	2 T04506	hypothetical prote
31	98.5	3.5	629	2 C64180	hypothetical prote
32	98.5	3.5	654	2 T14202	NADH2 dehydrogenas
33	98.5	3.5	699	2 F95146	DNA topoisomerase
34	98.5	3.5	701	2 D98014	DNA topoisomerase
35	98.5	3.5	746	2 T46821	sideophore recept
36	98.5	3.5	746	2 A95420	Rhizobactin r
37	98.5	3.5	1012	2 JC5925	membrane kiocho pr
38	98	3.4	465	2 T19113	hypothetical prote
39	98	3.4	716	1 C60008	RNA-directed RNA p
40	98	3.4	760	2 T34414	hypothetical prote
41	98	3.4	817	2 H75035	probable membrane
42	97.5	3.4	454	2 T20829	probable serine ca
43	97.5	3.4	511	2 S61166	probable membrane
44	97.5	3.4	604	2 E75119	hypothetical prote
45	97.5	3.4	804	2 G71546	probable DNA gyras

ALIGNMENTS

RESULT 1

UC7506
heparanase protein 2a - human
C/Species: Homo sapiens (man)
C/Date: 17-Nov-2000 #sequence_revision 17-Nov-2000 #text_change 09-Jul-2004
C/Accession: JC7506
R/McKenzie, E.; Tyson, K.; Stamps, A.; Smith, P.; Turner, P.; Barry, R.; Hircock, M.; Pat
Biochem. Biophys. Res. Commun. 276, 1170-1177, 2000
A/Title: Cloning and expression profiling of Hpa2, a novel mammalian heparanase family me
A/Reference number: JC7506
A/Accession: JC7506
A/Molecule type: mRNA
A/Residues: 1-480 <MCK>
A/Cross-references: UNIPROT:Q9HB39; GB:AF282885
C/Comment: This protein, a intracellular membrane-bound enzyme, has biological and therat
therapies.
C/Genetics:
A/Genes: hpa2a
A/Map position: 10q23-10q24
C/Keywords: heparin binding; membrane bound

Query Match	Best Local Similarity	Score	Pred. No.	Length	DB 2;	Length	DB 2;	Length	DB 2;
Matches	202;	Conservative	74;	Mismatches	146;	Indels	139;	Gaps	9;
QY	20	PLGRLSPGAL	-----PRPA-----QAQVVDIDFTQEPHLVSPS	55					
DB	18	PPACIAPGALYALALHLHLSLSSQAGRRPLPVDRAGLKEKTLILDVSTKDPRTVEN	77						
QY	56	PLSVTIDAMIDPRLILGSPKLTTLARGSPAYLRFQGTQDFLIF	-----DPKKEST	111					
DB	78	FSLQIDPSIITHD-GWLDPLSSKRLVTLARGSPALRGCGKRTDPLQONLRNPKSR	135						
QY	112	FEERSYQSQVQVNDICKYSSIPPDVEEKLRLMPYOQLLRHYYOKKRNSTYSSAVD	171						
DB	136	-----GAPGPD-----YLYKNYE-----	148						
QY	172	VLTPANCGLDILFGLNALLRTRADIQWSSNAQILLDYCSSKGYNISWELGNEPNSFLX	231						
DB	149	-----DEPNNYKT	156						
QY	232	KADIFNGSQLEGDYIQLHLRLK-STFKNAXLYGPDVQOPRRKTKMLKSLKAGGEVI	290						
DB	157	MGRAYVNSQLGKDYIQLKSLDPLRIYGRASLYGNIRPRKNVYALLDGFVKVAGSTV	216						
QY	291	DSVTIMHYLLNGTATREDPLNPDVDLIFISSVQKVFQVESTRPCKKVMLGTSAYGG	350						
DB	217	DAVTQHCYIDGRVVMKMPDLKTRILDTLSDQIRKIQKVVNTYTPCKKTIWLBGVVTSAG	276						
QY	351	GALLSDTPAAGFMIDKGLSARMGIEVVMRQVFEGAGNHYHVDNPPILPDYMLSLF	410						
DB	277	GTTNLSDSYAAAGFLMINTLIGMLANOGIDIVIRHSFPDHGYNHLVDONFNPDPYMLSLF	336						

Query Match 99.9%; Score 2838; DB 2; Length 543;
Best Local Similarity 99.8%; Pred. No. 6.2e-273;
Matches 542; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```
QY      1 MLRRKRALPPPLMLLLGLPLSPGALPRPAQADVLDLDFTOEPHLVSPSLSVT 60
DB      1 MLRRKRALPPPLMLLLGLPLSPGALPRPAQADVLDLDFTOEPHLVSPSLSVT 60
QY      61 IDANLATDPRFLILGSPKLTARGLSPAYLRFSGTKTDPLIFDPKKESTFEERSYMS 120
DB      61 IDANLATDPRFLILGSPKLTARGLSPAYLRFSGTKTDPLIFDPKKESTFEERSYMS 120
QY      121 QVNODICKYGSIPPDVEEKLRLMPYQEQLLREHYQKKFKNSTYGRSSVDVLYTPANC 180
DB      121 QVNODICKYGSIPPDVEEKLRLMPYQEQLLREHYQKKFKNSTYGRSSVDVLYTPANC 180
QY      181 GIDLIFGLNALRTADLQWSSNAOULLDYCSSKGYNISWELGNEPNSFLKADIFINGS 240
DB      181 GIDLIFGLNALRTADLQWSSNAOULLDYCSSKGYNISWELGNEPNSFLKADIFINGS 240
QY      241 QLGEDYIQLHKLIRKSTFGNAKLYGPDVGQPRKRTAKMLKSLKAGGEVIDSVTHHYTL 300
DB      241 QLGEDYIQLHKLIRKSTFGNAKLYGPDVGQPRKRTAKMLKSLKAGGEVIDSVTHHYTL 300
QY      301 NGRTATREDFLNPDVLDIFISSVQKVFQVESTPGKXWLGETSAYGGAPLSDTFA 360
DB      301 NGRTATREDFLNPDVLDIFISSVQKVFQVESTPGKXWLGETSAYGGAPLSDTFA 360
QY      361 AGFMWLDKLGSLARMGI EYVMRQVFFGAGNYHLDENFPLPDYMLSLFKKLVGTKVLM 420
DB      361 AGFMWLDKLGSLARMGI EYVMRQVFFGAGNYHLDENFPLPDYMLSLFKKLVGTKVLM 420
QY      421 ASVQSKRRKRLRYLHCTNTDNPRYKEGDLTYAINLHNVTXYLRLEYPFSNKQVDKXLL 480
DB      421 ASVQSKRRKRLRYLHCTNTDNPRYKEGDLTYAINLHNVTXYLRLEYPFSNKQVDKXLL 480
QY      481 RPLGPHGLLSKSVQNLGLTLKXVDDQTLPPLMKEPLRPGSSLGLPASYSFFVIRNAKYA 540
DB      481 RPLGPHGLLSKSVQNLGLTLKXVDDQTLPPLMKEPLRPGSSLGLPASYSFFVIRNAKYA 540
QY      541 ACI 543
DB      541 ACI 543
```

Search completed: March 23, 2005, 11:25:48
Job time : 117.5 secs

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XX  US2003217375-A1.
PN
XX
XX  20-NOV-2003.
PD
XX
XX  24-FEB-2003; 2003US-00371218.
PF
XX
XX  31-AUG-1998; 98WO-US017954.
PR  01-MAR-1999; 99US-00258892.
PR  06-FEB-2001; 2001US-00776874.
PR  19-NOV-2001; 2001US-00988113.
XX
XX  (ZCHARA/) ZCHARIA E.
PA  (VL0D/) VL0DAVSKY I.
PA  (METZ/) METZGER S.
PA  (PECK/) PECKER I.
PA  (ILAN/) ILAN N.
PA  (CHAU/) CHAUJER-SHAUL T.
PA  (GOLD/) GOLDSHMIDT O.
XX
XX  Zcharia E, Vlodaysky I, Metzger S, Pecker I, Ilan N;
PI  Chajek-Shaul T, Goldshmidt O;
DR  N-PSDB; ADM48719, ADM48721.
XX
XX  WPI: 2004-021918/02.
XX
XX  New transgenic non-human animal expressing heparinase, useful as models
PT  for human disease, such as cancers, viral infection, neurodegenerative
PT  diseases, restenosis, atherosclerosis and pulmonary disorders.
XX
XX  Example 6; SEQ ID NO 14; 106pp; English.
XX
XX  The present invention relates to a transgenic non-human animal whose
CC  genome comprises an exogenous polynucleotide sequence, including a
CC  promoter active in tissues of the non-human, a region encoding a human
CC  heparanase, where the promoter and the region encoding human heparanase
CC  are operably linked in the exogenous polynucleotide such that human
CC  heparanase is expressed in at least a portion of the cells of the non-
CC  human animal. The methods and compositions of the present invention are
CC  useful for the production of transgenic animals expressing heparanase, to
CC  be used as models for human diseases such as cancers, viral infection,
CC  restenosis, neurodegenerative diseases, atherosclerosis and pulmonary
CC  disorders. The present sequence is human SK-hepi hpa protein used in the
CC  exemplification of the invention.
XX
XX  Sequence 592 AA;
SQ
Query Match      100.0%; Score 2842; DB 8; Length 592;
Best Local Similarity 100.0%; Pred. No. 2.9e-273;
Matches 543; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

DB  350  NGRITATREDPLNDVLDIFISSVQKVFQVESTTRPGKVMLGFTSSAYGGANPLSDTFA 409
QY  361  AGFWMLDKLGLSARNGIEVYMRQVFFGAGNYHLVDENEDPLBDYMLSLFKKLVGTXYLM 420
DB  410  AGFWMLDKLGLSARNGIEVYMRQVFFGAGNYHLVDENEDPLBDYMLSLFKKLVGTXYLM 469
QY  421  ASVQGSKKRKRLRYVTHCNTNDNPRKEDDLTYAINLNHNTKYLALPPYFSKKQVDKXLL 480
DB  470  ASVQGSKKRKRLRYVTHCNTNDNPRKEDDLTYAINLNHNTKYLALPPYFSKKQVDKXLL 529
QY  481  RPLGPHGLSKSVOLNGTLTKWVDOTLPLMEKPLRPPSSGLPAPFSYFVIRNAKVA 540
DB  530  RPLGPHGLSKSVOLNGTLTKWVDOTLPLMEKPLRPPSSGLPAPFSYFVIRNAKVA 589
QY  541  ACT 543
DB  590  ACT 592

RESULT 15
AA17082
ID  AA17082 standard; protein; 543 AA.
XX
XX  AA17082;
AC
XX  21-JUL-1999 (first entry)
DT
XX
DE  Human heparanase enzyme.
XX
XX  Heparanase; endoglucuronidase; heparan sulfate proteoglycan; enzyme;
XX  metastasis; angiogenesis; wound healing; angioplasmy-induced restenosis;
XX  atherosclerosis; inflammation; tissue development;
XX  human; HSPG.
XX
XX  Homo sapiens.
OS
XX
XX  WO921975-A1.
PN
XX  06-MAY-1999.
PD
XX
XX  28-OCT-1998; 98WO-AU000898.
PF
XX
XX  28-OCT-1997; 97AU-00000062.
PR  09-DEC-1997; 97AU-00000812.
XX
XX  (AUSU ) UNIV AUSTRALIAN NAT.
PA
XX
XX  Freeman CG, Hulett MD, Parish CR, Hamdorf BJ;
PI  WPI: 1999-312956/26.
XX
XX  N-PSDB; AAX37259.
DR
XX
XX  Polynucleotides encoding mammalian endoglucuronidases, especially
PT  heparanases, useful to promote wound healing.
XX
XX  Claim 6; Page 69-73; 112pp; English.
XX
XX  The invention relates to nucleic acid sequences that encode heparanase
CC  enzymes having endoglucuronidase activity. Recombinant heparanases are
CC  capable of removing the HS side chain from heparan sulfate proteoglycan
CC  (HSPG). Sulfated oligosaccharides, sulphonates or HSPG can be used to
CC  inhibit heparanase, this is useful for treatment of a physiological or
CC  medical condition associated with elevated heparanase activity, such as
CC  metastasis, angiogenesis, wound healing, angioplasmy-induced restenosis,
CC  atherosclerosis, atherosclerosis and inflammation. The human, murine and
CC  rat heparanases can be used to enhance wound healing, especially
CC  associated with tissue development and repair. The conditions mentioned
CC  above can be diagnosed using specific antibodies, and also using primers
CC  and probes specific for the heparanase polynucleotides. Other uses of the
CC  heparanases include sequencing sulfated molecules such as HSPG. The
CC  present sequence represents a human heparanase
XX
XX  Sequence 543 AA;
SQ

```



```

QY 361 AGFMWLDKLGISARNGIEVVMRQVFPGAGNYHLVDENFDPLDPDWLSLLFKKLVGTKVLM 420
DB 410 AGFMWLDKLGISARNGIEVVMRQVFPGAGNYHLVDENFDPLDPDWLSLLFKKLVGTKVLM 469
QY 421 ASVQGSKRKRKLAVYLHCTNTDNPARYKSGDLTYALNLHVNTKYLRLPYPSNKKQVDKYL 480
DB 470 ASVQGSKRKRKLAVYLHCTNTDNPARYKSGDLTYALNLHVNTKYLRLPYPSNKKQVDKYL 529
QY 481 RPLGPHGLSKSVQNLGLTLKMWDDQTLPLMEKPLRPGSSISGLPAFSYSPFVIRNAKYA 540
DB 530 RPLGPHGLSKSVQNLGLTLKMWDDQTLPLMEKPLRPGSSISGLPAFSYSPFVIRNAKYA 589
QY 541 ACT 543
DB 590 ACT 592

RESULT 13
ADL16383
ID ADL16383 standard; protein; 592 AA.
XX
AC ADL16383;
XX
DT 06-MAY-2004 (first entry)
XX
DE Human heparanase full length protein.
XX
KM Human; heparanase; heparanase-dependent cancer; cancer;
XX autoimmune reaction; inflammation; chromosome 4; enzyme.
XX
OS Homo sapiens.
XX
PN US2003236215-A1.
XX
PD 25-DEC-2003.
XX
PF 09-JUN-2003; 2003US-00456573.
XX
PR 31-AUG-1998; 98MO-US017954.
PR 01-MAR-1999; 99US-00256892.
PR 08-NOV-1999; 99US-00435739.
XX
PA (INSI-) INSIGHT STRATEGY & MARKETING LTD.
PA (HADA-) HADASIT MEDICAL RES SERVICES & DEV.
XX
PI Pecker I, Vlodavsky I, Feinstein E;
XX
DR WPI; 2004-070610/07.
XX
PT New antisense oligonucleotide hybridizable with a polynucleotide encoding
PT a polypeptide with heparanase activity, useful for treating diseases such
PT as cancer and autoimmune disorders.
XX
PS Claim 3; SEQ ID NO 14; 108bp; English.
XX
CC The invention relates to an antisense oligonucleotide (ASO) comprising a
CC polynucleotide or a polynucleotide analogue of at least 10 bases being
CC hybridizable in vivo, under physiological conditions, with a portion of
CC a polynucleotide strand encoding a polypeptide having heparanase
CC catalytic activity. Also included are a method of in vivo downregulating
CC heparanase activity (comprising administering the ASO in vivo), a method
CC of treating a subject suffering from a pathological condition
CC (characterised by heparanase activity, comprising administering ASO to
CC the subject), a pharmaceutical composition comprising the ASO and a
CC carrier, an antisense nucleic acid construct (comprising a promoter
CC sequence and a polynucleotide sequence directing the synthesis of an
CC antisense RNA sequence of at least 10 bases being hybridizable in vivo),
CC under physiological conditions, with a polynucleotide strand encoding a
CC polypeptide having heparanase catalytic activity), a method of in vivo
CC downregulating heparanase activity (comprising administering in vivo the
CC antisense nucleic acid construct), a pharmaceutical composition
CC comprising the antisense nucleic acid construct and a carrier, and an
CC antisense oligonucleotide comprising a polynucleotide or a polynucleotide

```

```

CC analogue of at least 10 bases being hybridizable in vivo, under
CC physiological conditions, with a portion of a polynucleotide strand being
CC characterised by forming at least a portion of an untranslated region
CC (UTR) for a polynucleotide strand encoding a polypeptide having
CC heparanase catalytic activity. The methods and compositions of the
CC present invention are useful for the prevention and/or treatment of
CC diseases or conditions associated with aberrant heparanase activity, such
CC as heparanase-dependent cancer, cancer, autoimmune reaction and
CC inflammation. The gene for human heparanase is located on chromosome 4.
CC The present sequence is a human heparanase protein.
XX
SQ Sequence 592 AA;
Query Match 100.0%; Score 2842; DB 8; Length 592;
Best Local Similarity 100.0%; Pred. No. 2.9e-273;
Matches 543; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MLIRSKPALPPPLMLLLGPGSPGALPRPAQADVVDDFFPQEPHLVSPSFLSYT 60
DB 50 MLIRSKPALPPPLMLLLGPGSPGALPRPAQADVVDDFFPQEPHLVSPSFLSYT 109
QY 61 IDANLATPDRFLILGSPKLTARGLSPAYRFGGTQDPLIPDKKSTFEBSYWS 120
DB 110 IDANLATPDRFLILGSPKLTARGLSPAYRFGGTQDPLIPDKKSTFEBSYWS 169
QY 121 QVNODICKYGSIPDVEEKLRLMPYOBQLLREHYOKKFNKSTYSRSSVDVLYTFANCS 180
DB 170 QVNODICKYGSIPDVEEKLRLMPYOBQLLREHYOKKFNKSTYSRSSVDVLYTFANCS 229
QY 181 GIDLIFGLNALIRTDLDQNSSNAQLLDYCSSKGYNISWEIGNEPNSFLKKADIPIFINS 240
DB 230 GIDLIFGLNALIRTDLDQNSSNAQLLDYCSSKGYNISWEIGNEPNSFLKKADIPIFINS 289
QY 241 QLGEDYIOHLKLRSTFNKATLYGPDVGQPPRKATKSLFKXAGGEYIDSVTHHHYL 300
DB 290 QLGEDYIOHLKLRSTFNKATLYGPDVGQPPRKATKSLFKXAGGEYIDSVTHHHYL 349
QY 301 NGRTATREDPLNPVDLIFISSVQKVFQVESTRGKKVWLGETSSAYGGAPLLSDTPFA 360
DB 350 NGRTATREDPLNPVDLIFISSVQKVFQVESTRGKKVWLGETSSAYGGAPLLSDTPFA 409
QY 361 AGFMWLDKLGISARNGIEVVMRQVFPGAGNYHLVDENFDPLDPDWLSLLFKKLVGTKVLM 420
DB 410 AGFMWLDKLGISARNGIEVVMRQVFPGAGNYHLVDENFDPLDPDWLSLLFKKLVGTKVLM 469
QY 421 ASVQGSKRKRKLAVYLHCTNTDNPARYKSGDLTYALNLHVNTKYLRLPYPSNKKQVDKYL 480
DB 470 ASVQGSKRKRKLAVYLHCTNTDNPARYKSGDLTYALNLHVNTKYLRLPYPSNKKQVDKYL 529
QY 481 RPLGPHGLSKSVQNLGLTLKMWDDQTLPLMEKPLRPGSSISGLPAFSYSPFVIRNAKYA 540
DB 530 RPLGPHGLSKSVQNLGLTLKMWDDQTLPLMEKPLRPGSSISGLPAFSYSPFVIRNAKYA 589
QY 541 ACT 543
DB 590 ACT 592

RESULT 14
ADMA8720
ID ADMA8720 standard; protein; 592 AA.
XX
AC ADMA8720;
XX
DT 03-JUN-2004 (first entry)
XX
DE Human SK-hep1 hpa protein.
XX
KM Transgenic animal; heparanase; cancer; viral infection; restenosis;
XX neurodegenerative disease; atherosclerosis; pulmonary disorder; hpa;
XX human.
XX
OS Homo sapiens.

```

XX Claim 22; Page 122-123; 152pp; English.

PS The present sequence represents a human protein with heparanase catalytic
 CC activity. The heparanase (hpa) polynucleotide is useful in gene therapy,
 CC particularly in treating tumour, inflammation or autoimmunity.
 CC Particularly, the polynucleotide is useful in modulating the
 CC bioavailability of heparin-binding growth factors, cellular responses to
 CC heparin-binding growth factors (e.g. bFGF) and cytokines (e.g.
 CC interleukin (IL)-6), cell interaction with plasma lipoproteins, cellular
 CC susceptibility to certain viral and some bacterial and protozoa
 CC infections, or disintegration of neurodegenerative plaques. The
 CC polynucleotide is also useful in wound healing (e.g. thermal, chemical or
 CC radiation burns), and in the treatment of angiogenesis, restenosis,
 CC atherosclerosis, inflammation, neurodegenerative diseases (Gerstmann-
 CC Strausler Syndrome or Creutzfeldt-Jakob disease), and some viral,
 CC bacterial or protozoa infections

CC Sequence 592 AA;

SQ Query Match 100.0%; Score 2842; DB 3; Length 592;

Best Local Similarity 100.0%; Pred. No. 2.9e-273; Indels 0; Gaps 0;

Matches 543; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLRSKPALPPPLMLLLGLPLSPGALPRPAQADVVDLDFTEPHLVSPFLSVT 60
 DB MLRSKPALPPPLMLLLGLPLSPGALPRPAQADVVDLDFTEPHLVSPFLSVT 109
 QY IDANLATDRPFLILGSPKRLTLARGLSPAYLRFPGTKTDPLIFDPKKSSTFEERSYWS 120
 DB IDANLATDRPFLILGSPKRLTLARGLSPAYLRFPGTKTDPLIFDPKKSSTFEERSYWS 169
 QY 110 IDANLATDRPFLILGSPKRLTLARGLSPAYLRFPGTKTDPLIFDPKKSSTFEERSYWS 169
 DB 121 QVNMDCIKGSIPTDVEEKLRLLEMPYQEOULLREHYQKFKNSTYRSASVDVLYTPANCS 180
 170 QVNMDCIKGSIPTDVEEKLRLLEMPYQEOULLREHYQKFKNSTYRSASVDVLYTPANCS 229
 QY 181 GLDLIFGLNALRTADLQWNSNAQLLDYCSSKGYNISWELGNEBNSFLKADIFINGS 240
 DB GLDLIFGLNALRTADLQWNSNAQLLDYCSSKGYNISWELGNEBNSFLKADIFINGS 289
 QY 230 GLDLIFGLNALRTADLQWNSNAQLLDYCSSKGYNISWELGNEBNSFLKADIFINGS 289
 DB 241 QUGEDYIQLHKLKRSKTFPKNAKLYGPDVQOPRKRTAKMLKSLKAGGEVIDSTVTHHHYLL 300
 290 QUGEDYIQLHKLKRSKTFPKNAKLYGPDVQOPRKRTAKMLKSLKAGGEVIDSTVTHHHYLL 349
 QY 301 NGRTATREDPLNDVDLDFISSVQKVFQVVESTRPGKRWLGFTSSAYGGAPLSDTFA 360
 DB NGRTATREDPLNDVDLDFISSVQKVFQVVESTRPGKRWLGFTSSAYGGAPLSDTFA 409
 QY 361 AGFMWLDKLGSLARMGIEVVMROVFFGAGNYHLVDENFDPLPDYMLSLLEFKLVGTVLM 420
 DB AGFMWLDKLGSLARMGIEVVMROVFFGAGNYHLVDENFDPLPDYMLSLLEFKLVGTVLM 469
 QY 421 ASVQSGRRRLRYLHCTNTDNPRYKEGDLTYALINANTKTLRLPYPPSNQVDKYL 480
 DB ASVQSGRRRLRYLHCTNTDNPRYKEGDLTYALINANTKTLRLPYPPSNQVDKYL 529
 QY 481 RPLGPHGLSKSVQNLGLTLKMWDDOTLPLMEKPLRPGSSGLPAFYSYFFVIRNAKVA 540
 DB RPLGPHGLSKSVQNLGLTLKMWDDOTLPLMEKPLRPGSSGLPAFYSYFFVIRNAKVA 589
 QY 541 ACI 543
 DB 590 ACI 592

RESULT 12

ADG88804

ID ADG88804 standard; protein: 592 AA.

XX ADG88804;

XX ADG88804;

DT 11-MAR-2004 (first entry)

DE Human SK-hep1 protein.

XX Wound healing; heparanase; ulcer; burn; laceration; surgical incision;
 KW necrosis; pressure wound; diabetic ulcer; angiogenesis; human; therapy.

XX Homo sapiens.

XX US2003161823-A1.

XX 28-AUG-2003.

XX 14-JAN-2003; 2003US-00341582.

XX 31-AUG-1998; 98WO-US017954.

XX 01-MAR-1999; 99US-00258892.

XX 06-FEB-2001; 2001US-00776874.

XX 05-SEP-2001; 2001WO-1L000830.

XX 19-NOV-2001; 2001US-00988113.

XX (ILAN/) ILAN N.

XX (VLOD/) VLODAVSKY I.

XX (YACO/) YACOBY-ZEEVI O.

XX (PECK/) PECKER I.

XX (FEIN/) FEINSTEIN E.

XX Ilan N, Vlodavsky I, Yacoby-Zeevi O, Pecker I, Feinstein E;

XX WPI: 2003-897910/82.

XX N-PSDB; ADG88803, ADG88805.

XX Composition for treating a wound comprising recombinant heparanase is

XX useful to induce or accelerate wound healing and induce or accelerate

XX angiogenesis.

XX Claim 2; SEQ ID NO 14; 143pp; English.

XX The present invention relates to methods and compositions for inducing

XX CC and/or accelerating wound healing via the catalytic activity of

XX CC heparanase. The invention is used to induce or accelerate a healing

XX CC process, particularly of an ulcer, burn, laceration, surgical incision,

XX CC necrosis, pressure wound, diabetic ulcer and to induce or accelerate

XX CC angiogenesis. The present sequence is human SK-hep1 protein.

XX Sequence 592 AA;

SQ Query Match 100.0%; Score 2842; DB 7; Length 592;

Best Local Similarity 100.0%; Pred. No. 2.9e-273; Indels 0; Gaps 0;

Matches 543; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLRSKPALPPPLMLLLGLPLSPGALPRPAQADVVDLDFTEPHLVSPFLSVT 60
 DB MLRSKPALPPPLMLLLGLPLSPGALPRPAQADVVDLDFTEPHLVSPFLSVT 109
 QY IDANLATDRPFLILGSPKRLTLARGLSPAYLRFPGTKTDPLIFDPKKSSTFEERSYWS 120
 DB IDANLATDRPFLILGSPKRLTLARGLSPAYLRFPGTKTDPLIFDPKKSSTFEERSYWS 169
 QY 110 IDANLATDRPFLILGSPKRLTLARGLSPAYLRFPGTKTDPLIFDPKKSSTFEERSYWS 169
 DB 121 QVNMDCIKGSIPTDVEEKLRLLEMPYQEOULLREHYQKFKNSTYRSASVDVLYTPANCS 180
 170 QVNMDCIKGSIPTDVEEKLRLLEMPYQEOULLREHYQKFKNSTYRSASVDVLYTPANCS 229
 QY 181 GLDLIFGLNALRTADLQWNSNAQLLDYCSSKGYNISWELGNEBNSFLKADIFINGS 240
 DB GLDLIFGLNALRTADLQWNSNAQLLDYCSSKGYNISWELGNEBNSFLKADIFINGS 289
 QY 230 GLDLIFGLNALRTADLQWNSNAQLLDYCSSKGYNISWELGNEBNSFLKADIFINGS 289
 DB 241 QUGEDYIQLHKLKRSKTFPKNAKLYGPDVQOPRKRTAKMLKSLKAGGEVIDSTVTHHHYLL 300
 290 QUGEDYIQLHKLKRSKTFPKNAKLYGPDVQOPRKRTAKMLKSLKAGGEVIDSTVTHHHYLL 349
 QY 301 NGRTATREDPLNDVDLDFISSVQKVFQVVESTRPGKRWLGFTSSAYGGAPLSDTFA 360
 DB NGRTATREDPLNDVDLDFISSVQKVFQVVESTRPGKRWLGFTSSAYGGAPLSDTFA 409

QY 541 ACI 543
|||
DB 541 ACT 543

RESULT 10

AAV02346
ID AAV02346 standard; protein; 592 AA.

AC AAV02346;

DT 09-JUL-1999 (first entry)

DE A human heparanase protein.

KW Heparanase; hpa; modulator; heparin-binding growth factor;
cellular response; cytokine; cell interaction; plasma lipoprotein;
cellular susceptibility; infection; disintegration;
neurodegenerative plaque; wound healing; angiogenesis; restenosis;
atherosclerosis; inflammation; neurodegenerative disease; neutralise;
plasma heparin; micrometastasis; autoimmune lesion; renal failure.

OS Homo sapiens.

PN W09911798-A1.

PD 11-MAR-1999.

PF 31-AUG-1998; 98WO-US017954.

PR 02-SEP-1997; 97US-00922170.

PR 02-JUL-1998; 98US-00109386.

PA (INSI-) INSIGHT STRATEGY & MARKETING LTD.
(HADA-) HADASIT MEDICAL RES SERVICES & DEV.
(FRIE/) FRIEDMAN M M.

PI Pecker I, Vlodavsky I, Feinstein E;

DR WPI: 1999-102255/25.

DR N-PSDB; AAV35650.

PT New human polynucleotide useful for treating angiogenesis, restenosis,
and inflammation.

PS Claim 6; Page 65-66; 63pp; English.

XX The specification describes a polypeptide having heparanase (hpa)
activity. The recombinant protein is used as a modulator of heparin-
binding growth factors, cellular responses to heparin-binding growth
factors and cytokines, cell interaction with plasma lipoproteins,
cellular susceptibility to viral, protozoal and bacterial infections or
disintegration of neurodegenerative plaques. Heparanase may be useful for
conditions such as wound healing, angiogenesis, restenosis,
atherosclerosis, inflammation, neurodegenerative diseases, and viral
infections. Mammalian heparanase can be used to neutralize plasma
heparin, and anti-heparanase antibodies may be applied for
immunodetection and diagnosis of micrometastases, autoimmune lesions, and
renal failure in biopsy specimens, plasma samples, and body fluids. The
present sequence represents human heparanase

XX SQ Sequence 592 AA;

Query Match 100.0%; Score 2842; DB 2; Length 592;

Best Local Similarity 100.0%; Pred. No. 2.9e-273; Indels 0; Gaps 0;

Matches 543; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLRSKPAIPPLMLLLGLGPGALPPPAQADVVDLFFTOEPHLVSPFLSYT 60

DB 50 MLRSKPAIPPLMLLLGLGPGALPPPAQADVVDLFFTOEPHLVSPFLSYT 109

QY 61 IDANLATDPRFLILGSPKLTARGLSPAYLRFGGXTDPLFDPKKESTFEERSYWS 120

DB 110 IDANLATDPRFLILGSPKLTARGLSPAYLRFGGXTDPLFDPKKESTFEERSYWS 169

QY 121 QVNODICXGYSIPDVEEKLRLRLEMPYOBQLLRHRYOKFKNSTYRSASVDLYTFANCS 180

DB 170 QVNODICXGYSIPDVEEKLRLRLEMPYOBQLLRHRYOKFKNSTYRSASVDLYTFANCS 229

QY 181 GIDLIFGNALLRLTADLQWSSNAQLLDYCSKGYNISWEIGNEPNSFLKXADIFINGS 240

DB 230 GIDLIFGNALLRLTADLQWSSNAQLLDYCSKGYNISWEIGNEPNSFLKXADIFINGS 289

QY 241 QIGEDYIQLHKILRSTFKNAKLYGPDVGOPRRRTAKMLKSLKAGGVISVTMHHYLL 300

DB 290 QIGEDYIQLHKILRSTFKNAKLYGPDVGOPRRRTAKMLKSLKAGGVISVTMHHYLL 349

QY 301 NGRTATREDPLNPVDLDFISSVQKVPQVVESTRPGKYLWGETSSAYAGGAPLSDTFA 360

DB 350 NGRTATREDPLNPVDLDFISSVQKVPQVVESTRPGKYLWGETSSAYAGGAPLSDTFA 409

QY 361 AGFWMLDKLGISARNGIEVVMKQVFFGAGNYHLVDENFDPLDYWLSLFFKLVGTXYLM 420

DB 410 AGFWMLDKLGISARNGIEVVMKQVFFGAGNYHLVDENFDPLDYWLSLFFKLVGTXYLM 469

QY 421 ASVQSSKRRKRLRVYLHCTNTDNPRLKEGDLTYAINLNNVTYLLPYPFSNKQVDKYL 480

DB 470 ASVQSSKRRKRLRVYLHCTNTDNPRLKEGDLTYAINLNNVTYLLPYPFSNKQVDKYL 529

QY 481 RPLGPHGLSKSVQNLGLTLKRVDDQTLPLMEKELRPGSSIGLPAFSYFVINAKYA 540

DB 530 RPLGPHGLSKSVQNLGLTLKRVDDQTLPLMEKELRPGSSIGLPAFSYFVINAKYA 589

QY 541 ACT 543

DB 590 ACT 592

RESULT 11

AAV08850
ID AAV08850 standard; protein; 592 AA.

AC AAV08850;

DT 15-JAN-2001 (first entry)

DE Amino acid sequence of a human heparanase polypeptide.

XX Human; heparanase; gene therapy; tumour; inflammation; autoimmunity;
heparin-binding growth factor; cytokine; neurodegenerative plaque;
wound healing; infection; burn; angiogenesis; restenosis;
atherosclerosis; inflammation; neurodegenerative disease;
Gerstmann-Strausler Syndrome; Creutzfeldt-Jakob disease.

OS Homo sapiens.

PN W0200052178-A1.

PD 08-SEP-2000.

PF 14-FEB-2000; 2000WO-US003542.

PR 01-MAR-1999; 99US-00258892.

PA (INSI-) INSIGHT STRATEGY & MARKETING LTD.
(HADA-) HADASIT MEDICAL RES SERVICES & DEV.
(FRIE/) FRIEDMAN M M.

PI Pecker I, Vlodavsky I, Feinstein E;

DR WPI: 2000-579289/54.

DR N-PSDB; AAV75053.

PT New polynucleotides encoding a polypeptide having heparanase activity,
useful in wound healing and in gene therapy, particularly in treating
tumour, inflammation, autoimmunity, neurodegenerative diseases.

Best Local Similarity 100.0%; Pred. No. 2,5e-273;
Matches 543; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 MLRSKPALPPMLMLLLGPGPLSPGALPRPAQADVDVLDFFTOEPLHLVSPFLSVT 60
DB 1 MLRSKPALPPMLMLLLGPGPLSPGALPRPAQADVDVLDFFTOEPLHLVSPFLSVT 60
QY 61 IDANLATDPRFLILGSPKLTARGLSPAYLRFGGKTDFLIPDKKESTEESSYMS 120
DB 61 IDANLATDPRFLILGSPKLTARGLSPAYLRFGGKTDFLIPDKKESTEESSYMS 120
QY 121 QVNODICKYGSIPDVEEKLRLWPYQEQLLREHYQKKFKNSTYSSRSSVDVLYTFPANC 180
DB 121 QVNODICKYGSIPDVEEKLRLWPYQEQLLREHYQKKFKNSTYSSRSSVDVLYTFPANC 180
QY 181 GDDLIFGLNALRLTADLQWSSNAQLLDYCSSKGYNISWELGNEPNSFLKADIFINGS 240
DB 181 GDDLIFGLNALRLTADLQWSSNAQLLDYCSSKGYNISWELGNEPNSFLKADIFINGS 240
QY 241 QUGEDYIQLHKLRLKSTFKNAKLYGPDVGQPRKTKAKMLKSLKAGGEVIDSVTHHYLL 300
DB 241 QUGEDYIQLHKLRLKSTFKNAKLYGPDVGQPRKTKAKMLKSLKAGGEVIDSVTHHYLL 300
QY 301 NGRTATREDPLNDVLDIFISSVQKVFQVVESTRPCKKVMLGETSAYGGAPLISDTPA 360
DB 301 NGRTATREDPLNDVLDIFISSVQKVFQVVESTRPCKKVMLGETSAYGGAPLISDTPA 360
QY 361 AGFMWLDKLGSLRWGIEVVMQVFFGAQNYHLVDENPDLDPYWSLLFKKLVGTVLM 420
DB 361 AGFMWLDKLGSLRWGIEVVMQVFFGAQNYHLVDENPDLDPYWSLLFKKLVGTVLM 420
QY 421 ASVQSGKRRKRLRYLHCTNTDNPYKESGDLTYAIVLHVTYKLRPYPSNKQVDKYL 480
DB 421 ASVQSGKRRKRLRYLHCTNTDNPYKESGDLTYAIVLHVTYKLRPYPSNKQVDKYL 480
QY 481 RPLGPHGLSKSVQVNLGLTLKAVDDOTLPLMEKPLRPSSSLGLPAFSYSFVIRNAKYA 540
DB 481 RPLGPHGLSKSVQVNLGLTLKAVDDOTLPLMEKPLRPSSSLGLPAFSYSFVIRNAKYA 540
QY 541 ACT 543
DB 541 ACT 543

RESULT 9
ADM48716
ID ADM48716 standard; protein; 543 AA.
XX
AC ADM48716;
XX
DT 03-JUN-2004 (first entry)
XX
DE Human hpa protein #1.
XX
KW Transgenic animal; heparanase; cancer; viral infection; restenosis;
KW neurodegenerative disease; atherosclerosis; pulmonary disorder; hpa;
KW human.
XX
OS Homo sapiens.
XX
PN US2003217375-A1.
XX
PD 20-NOV-2003.
XX
PF 24-FEB-2003; 2003US-00371218.
XX
PR 31-AUG-1998; 98WO-US017954.
PR 01-MAR-1999; 99US-00258892.
PR 06-FEB-2001; 2001US-00776874.
PR 19-NOV-2001; 2001US-00988113.
XX
XX (ZCHA/) ZCHARIA E.
PA (VL0D/) VL0DAVSKY I.

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PA (METZ/) METZGER S.
PA (PECK/) PECKER I.
PA (ILAN/) ILAN N.
PA (ZHAJ/) CHAJEK-SHAUL T.
PA (GOLD/) GOLDSMIDT O.

PI Zcharia E, Vl0davsky I, Metzger S, Pecker I, Ilan N,
PI Chajek-Shaul T, Goldsmidt O;
PI MPI: 2004-021918/02.

DR N-PSDB; ADM48715, ADM48717.

PT New transgenic non-human animal expressing heparinase, useful as models
PT for human disease, such as cancer, viral infection, neurodegenerative
PT diseases, restenosis, atherosclerosis and pulmonary disorders.

PS Example 1; SEQ ID NO 10; 106pp; English.

CC The present invention relates to a transgenic non-human animal whose
CC genome comprises an exogenous polynucleotide sequence, including a
CC promoter active in tissues of the non-human, a region encoding a human
CC heparanase, where the promoter and the region encoding human heparanase
CC are operably linked in the exogenous polynucleotide such that human
CC heparanase is expressed in at least a portion of the cells of the non-
CC human animal. The methods and compositions of the present invention are
CC useful for the production of transgenic animals expressing heparanase, to
CC be used as models for human diseases such as cancer, viral infection,
CC restenosis, neurodegenerative diseases, atherosclerosis and pulmonary
CC disorders. The present sequence is human hpa protein used in the
CC exemplification of the invention.

Sequence 543 AA;

Query Match 100.0%; Score 2842; DB 8; Length 543;

Best Local Similarity 100.0%; Pred. No. 2,5e-273;
Matches 543; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 MLRSKPALPPMLMLLLGPGPLSPGALPRPAQADVDVLDFFTOEPLHLVSPFLSVT 60
DB 1 MLRSKPALPPMLMLLLGPGPLSPGALPRPAQADVDVLDFFTOEPLHLVSPFLSVT 60
QY 61 IDANLATDPRFLILGSPKLTARGLSPAYLRFGGKTDFLIPDKKESTEESSYMS 120
DB 61 IDANLATDPRFLILGSPKLTARGLSPAYLRFGGKTDFLIPDKKESTEESSYMS 120
QY 121 QVNODICKYGSIPDVEEKLRLWPYQEQLLREHYQKKFKNSTYSSRSSVDVLYTFPANC 180
DB 121 QVNODICKYGSIPDVEEKLRLWPYQEQLLREHYQKKFKNSTYSSRSSVDVLYTFPANC 180
QY 181 GDDLIFGLNALRLTADLQWSSNAQLLDYCSSKGYNISWELGNEPNSFLKADIFINGS 240
DB 181 GDDLIFGLNALRLTADLQWSSNAQLLDYCSSKGYNISWELGNEPNSFLKADIFINGS 240
QY 241 QUGEDYIQLHKLRLKSTFKNAKLYGPDVGQPRKTKAKMLKSLKAGGEVIDSVTHHYLL 300
DB 241 QUGEDYIQLHKLRLKSTFKNAKLYGPDVGQPRKTKAKMLKSLKAGGEVIDSVTHHYLL 300
QY 301 NGRTATREDPLNDVLDIFISSVQKVFQVVESTRPCKKVMLGETSAYGGAPLISDTPA 360
DB 301 NGRTATREDPLNDVLDIFISSVQKVFQVVESTRPCKKVMLGETSAYGGAPLISDTPA 360
QY 361 AGFMWLDKLGSLRWGIEVVMQVFFGAQNYHLVDENPDLDPYWSLLFKKLVGTVLM 420
DB 361 AGFMWLDKLGSLRWGIEVVMQVFFGAQNYHLVDENPDLDPYWSLLFKKLVGTVLM 420
QY 421 ASVQSGKRRKRLRYLHCTNTDNPYKESGDLTYAIVLHVTYKLRPYPSNKQVDKYL 480
DB 421 ASVQSGKRRKRLRYLHCTNTDNPYKESGDLTYAIVLHVTYKLRPYPSNKQVDKYL 480
QY 481 RPLGPHGLSKSVQVNLGLTLKAVDDOTLPLMEKPLRPSSSLGLPAFSYSFVIRNAKYA 540
DB 481 RPLGPHGLSKSVQVNLGLTLKAVDDOTLPLMEKPLRPSSSLGLPAFSYSFVIRNAKYA 540

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PR 01-MAR-1999; 99US-00258892.
PR 06-FEB-2001; 2001US-0076874.
PR 05-SEP-2001; 2001WO-11000830.
PR 19-NOV-2001; 2001US-00988113.
XX
XX (ILAN/) ILAN N.
XX (VLAD/) VLADAVSKY I.
XX (YACOB/) YACOBY-ZEEVI O.
XX (PECK/) PECKER I.
XX (FEIN/) FEINSTEIN E.
XX
XX Ilan N, Vladavsky I, Yacoby-Zeevi O, Pecker I, Feinstein E;
XX
XX DR MPI: 2003-897910/82.
XX N-PSDB; ADG88799, ADG88801, ADG88832.
XX
XX Composition for creating a wound comprising recombinant heparanase is
XX useful to induce or accelerate wound healing and induce or accelerate
XX angiogenesis.
XX
XX Claim 2; SEQ ID NO 10; 143bp; English.
XX
XX The present invention relates to methods and compositions for inducing
XX and/or accelerating wound healing via the catalytic activity of
XX heparanase. The invention is used to induce or accelerate a healing
XX process, particularly of an ulcer, burn, laceration, surgical incision,
XX necrosis, pressure wound, diabetic ulcer and to induce or accelerate
XX angiogenesis. The present sequence is human hpa protein.
XX
XX SQ Sequence 543 AA;
XX
XX Query Match 100.0%; Score 2842; DB 7; Length 543;
XX Best Local Similarity 100.0%; Pred. No. 2, 5e-273; Indels 0; Gaps 0;
XX Matches 543; Conservative 0; Mismatches 0;
XX
XX 1 MLIRSKPALPPLMLLLPLGLSPGALPRPAQADVVLDLDFTEGPHLVSPFLSVT 60
XX 1 MLIRSKPALPPLMLLLPLGLSPGALPRPAQADVVLDLDFTEGPHLVSPFLSVT 60
XX
XX 61 IDANLATDRPFLILGSPKRLTLARGLSPAYLRFSGTKTDFLIPDKKSTPEERSYMS 120
XX 61 IDANLATDRPFLILGSPKRLTLARGLSPAYLRFSGTKTDFLIPDKKSTPEERSYMS 120
XX
XX 121 QVNODICKGSIIPDVEEKLRLEMPYQEOULLREHIOKKFKNSTYRSRVYDLYTFRANS 180
XX 121 QVNODICKGSIIPDVEEKLRLEMPYQEOULLREHIOKKFKNSTYRSRVYDLYTFRANS 180
XX
XX 121 QVNODICKGSIIPDVEEKLRLEMPYQEOULLREHIOKKFKNSTYRSRVYDLYTFRANS 180
XX 121 QVNODICKGSIIPDVEEKLRLEMPYQEOULLREHIOKKFKNSTYRSRVYDLYTFRANS 180
XX
XX 181 GLDLIFGLNALIRTDALQWNSSNAQLLLDYCSSKGYNISWELGNEPNSFLKADIPINGS 240
XX 181 GLDLIFGLNALIRTDALQWNSSNAQLLLDYCSSKGYNISWELGNEPNSFLKADIPINGS 240
XX
XX 241 QUGEDYIOHKLIRKSTFKNAKLYGPDVQPRKTKAKMLKSPFKAGGEYIDSTVMHHYVL 300
XX 241 QUGEDYIOHKLIRKSTFKNAKLYGPDVQPRKTKAKMLKSPFKAGGEYIDSTVMHHYVL 300
XX
XX 241 QUGEDYIOHKLIRKSTFKNAKLYGPDVQPRKTKAKMLKSPFKAGGEYIDSTVMHHYVL 300
XX 241 QUGEDYIOHKLIRKSTFKNAKLYGPDVQPRKTKAKMLKSPFKAGGEYIDSTVMHHYVL 300
XX
XX 301 NGRTATREDPLNDVDLFISSVQKFOVVESTRPKKTKWLGTSAYGGAAPLSDTPA 360
XX 301 NGRTATREDPLNDVDLFISSVQKFOVVESTRPKKTKWLGTSAYGGAAPLSDTPA 360
XX
XX 301 NGRTATREDPLNDVDLFISSVQKFOVVESTRPKKTKWLGTSAYGGAAPLSDTPA 360
XX 301 NGRTATREDPLNDVDLFISSVQKFOVVESTRPKKTKWLGTSAYGGAAPLSDTPA 360
XX
XX 361 AGFMWLDKLGSRMGIEVVMRQVFFGAGNYHLDENFPLPDYMLSLFKKLVTGKVLV 420
XX 361 AGFMWLDKLGSRMGIEVVMRQVFFGAGNYHLDENFPLPDYMLSLFKKLVTGKVLV 420
XX
XX 421 ASVQSKRRKRLRYLHCTNTDNRPRYEGDLTYAIVLHNVTKLRLPYPPSNQVVDKYL 480
XX 421 ASVQSKRRKRLRYLHCTNTDNRPRYEGDLTYAIVLHNVTKLRLPYPPSNQVVDKYL 480
XX
XX 421 ASVQSKRRKRLRYLHCTNTDNRPRYEGDLTYAIVLHNVTKLRLPYPPSNQVVDKYL 480
XX 421 ASVQSKRRKRLRYLHCTNTDNRPRYEGDLTYAIVLHNVTKLRLPYPPSNQVVDKYL 480
XX
XX 481 RPLGPGILSKSVQNLGLTKWVDQTLPLPMEKPLRPGSSGLPAPFSYFFYIRAKYA 540
XX 481 RPLGPGILSKSVQNLGLTKWVDQTLPLPMEKPLRPGSSGLPAPFSYFFYIRAKYA 540
XX
XX 481 RPLGPGILSKSVQNLGLTKWVDQTLPLPMEKPLRPGSSGLPAPFSYFFYIRAKYA 540
XX 481 RPLGPGILSKSVQNLGLTKWVDQTLPLPMEKPLRPGSSGLPAPFSYFFYIRAKYA 540
XX
XX 541 ACT 543
XX |||

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DB 541 ACT 543
XX
XX RESULT 8
XX ADL16379
XX ID ADL16379 standard; protein; 543 AA.
XX
XX AC ADL16379;
XX
XX DT 06-MAY-2004 (first entry)
XX
XX DE Human heparanase partial protein.
XX
XX KW Human; heparanase; heparanase-dependent cancer; cancer;
XX autoimmune reaction; inflammation; chromosome 4; enzyme.
XX
XX OS Homo sapiens.
XX
XX PN US2003236215-A1.
XX
XX PD 25-DEC-2003.
XX
XX PF 09-JUN-2003; 2003US-00456573.
XX
XX PR 31-AUG-1998; 98WO-US017954.
XX PR 01-MAR-1999; 99US-00258892.
XX PR 08-NOV-1999; 99US-00435739.
XX
XX (INSI-) INSIGHT STRATEGY & MARKETING LTD.
XX (HADA-) HADASIT MEDICAL RES SERVICES & DEV.
XX
XX Pecker I, Vladavsky I, Feinstein E;
XX
XX MPI: 2004-070610/07.
XX
XX PT New antisense oligonucleotide hybridizable with a polynucleotide encoding
XX a polypeptide with heparanase activity, useful for treating diseases such
XX as cancer and autoimmune disorders.
XX
XX PS Claim 3; SEQ ID NO 10; 108bp; English.
XX
XX The invention relates to an antisense oligonucleotide (ASO) comprising a
XX polynucleotide or a polynucleotide analogue of at least 10 bases being
XX hybridizable in vivo, under physiological conditions, with a portion of
XX a polynucleotide strand encoding a polypeptide having heparanase
XX catalytic activity. Also included are a method of in vivo downregulating
XX heparanase activity (comprising administering the ASO in vivo), a method
XX of treating a subject suffering from a pathological condition
XX (characterised by heparanase activity, comprising administering ASO to
XX the subject), a pharmaceutical composition comprising the ASO and a
XX carrier, an antisense nucleic acid construct (comprising a promoter
XX sequence and a polynucleotide sequence directing the synthesis of an
XX antisense RNA sequence of at least 10 bases being hybridizable in vivo,
XX under physiological conditions, with a polynucleotide strand encoding a
XX polypeptide having heparanase catalytic activity), a method of in vivo
XX downregulating heparanase activity (comprising administering in vivo the
XX antisense nucleic acid construct), a pharmaceutical composition
XX comprising the antisense nucleic acid construct and a carrier, and an
XX antisense oligonucleotide comprising a polynucleotide or a polynucleotide
XX analogue of at least 10 bases being hybridizable in vivo, under
XX physiological conditions, with a portion of a polynucleotide strand being
XX characterised by forming at least a portion of an untranslated region
XX (UTR) for a polynucleotide strand encoding a polypeptide having
XX heparanase catalytic activity. The methods and compositions of the
XX present invention are useful for the prevention and/or treatment of
XX diseases or conditions associated with aberrant heparanase activity, such
XX as heparanase-dependent cancer, cancer, autoimmune reaction and
XX inflammation. The gene for human heparanase is located on chromosome 4.
XX
XX The present sequence is a human heparanase protein.
XX
XX SQ Sequence 543 AA;
XX
XX Query Match 100.0%; Score 2842; DB 8; Length 543;

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Db      241 QLGEDYIQLHKLRLKSTFKNAKLYGPDVGQPRRTAKMKLSFLKAGGEVIDSVTMHHYYL 300
Qy      301 NGRTATREDPLNDVLDIFISSVQKVFQVVESTRGKKVWLGETSSAYGGAPLLSDTPA 360
Db      301 NGRTATREDPLNDVLDIFISSVQKVFQVVESTRGKKVWLGETSSAYGGAPLLSDTPA 360
Qy      361 AGFWMLDKLGLSARMGIEVVMRQVFEGAGNYHLVDENPDLDPDWLSLFLFKLVGTXYLM 420
Db      361 AGFWMLDKLGLSARMGIEVVMRQVFEGAGNYHLVDENPDLDPDWLSLFLFKLVGTXYLM 420
Qy      421 ASVQSSKRRKRLRVYLHCTNTDNPXYKEGDLTYAINTLHNTYKYLRLPYPSNKOVDKXYL 480
Db      421 ASVQSSKRRKRLRVYLHCTNTDNPXYKEGDLTYAINTLHNTYKYLRLPYPSNKOVDKXYL 480
Qy      481 RPLGPHGLSKSVQVNLGLTLKXVDDQTLPLMEKPLRPSSSLGLPAFSYSPFVIRAKYA 540
Db      481 RPLGPHGLSKSVQVNLGLTLKXVDDQTLPLMEKPLRPSSSLGLPAFSYSPFVIRAKYA 540
Qy      541 ACT 543
Db      541 ACT 543

RESULT 6
AB07813
ID      AB07813 standard; protein; 543 AA.
XX      AC      AB07813;
XX      XX      03-JUL-2002 (first entry)
DE      Human heparanase sequence.
DE      Heparanase; catalytic; cytosolic; antiviral; antibacterial; enzyme;
KW      anti-protocan; neuroprotective; heparin; human.
XX      OS      Homo sapiens.
XX      FH      Key      Location/Qualifiers
FT      Peptide      1..35
FT      Protein      /note="signal peptide"
FT      Protein      36..543
FT      Protein      /note="mature protein"
XX      US2002034810-A1.
XX      PD      21-MAR-2002.
XX      PF      16-AUG-2001; 2001US-00930218.
XX      PR      20-SEP-2000; 2000US-00666390.
XX      PA      (INSI-) INSIGHT STRATEGY & MARKETING LTD.
XX      PI      Goldschmidt O, Pecker I, Vlodavsky I, Michal I, Zcharia E;
XX      DR      WPI; 2002-338926/37.
XX      PT      Nucleic acid encoding avian and reptile heparanase polypeptide is useful
XX      PT      to treat various heparin-related disorders and the signal peptide is
XX      PT      useful in production of membrane-targeted or secreted recombinant
XX      PT      proteins.
XX      PS      Disclosure; Fig 1a; 39pp; English.
XX      CC      The invention relates to an isolated avian and reptile nucleic acid,
XX      CC      encoding a polypeptide with heparanase catalytic activity. The signal
XX      CC      peptide of the nucleic acid can be used to express membrane-associated or
XX      CC      secreted proteins in heterologous expression systems. The encoded
XX      CC      polypeptides can be used to prevent tumour angiogenesis, metastasis and
XX      CC      invasion, and to intervene with pathologies associated with impaired
XX      CC      heparin-binding growth factors, cellular responses to heparin-binding
XX      CC      growth factors and cytokines, cell interaction with plasma lipoproteins,

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CC      cellular susceptibility to viral, protozoa and bacterial infections or
CC      disintegration of neurodegenerative plaques. The present sequence
CC      represents a human heparanase protein sequence used in similarity studies
XX      XX
SQ      Sequence 543 AA;
Query Match      100.0%; Score 2842; DB 5; Length 543;
Best Local Similarity 100.0%; Pred. No. 2.56-273;
Matches 543; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
1 MLRSKPLPPLMLLLGLGELSPGALPRPAQADVDDLPFQEPHLHVSPLSYT 60
Db      1 MLRSKPLPPLMLLLGLGELSPGALPRPAQADVDDLPFQEPHLHVSPLSYT 60
Qy      61 IDANLATDPRFLILGSPRLTARGLSPAYLRFQGTDTPLIPDKKSTEESSYWS 120
Db      61 IDANLATDPRFLILGSPRLTARGLSPAYLRFQGTDTPLIPDKKSTEESSYWS 120
Qy      121 QVNODICRYGSLPPDVEEKLRLWEPIYQQLLRHHYQKKFKNSTYSRSSVDVLYTFANCS 180
Db      121 QVNODICRYGSLPPDVEEKLRLWEPIYQQLLRHHYQKKFKNSTYSRSSVDVLYTFANCS 180
Qy      181 GLDLIFGLNALIRTDADLQWNSNAQLLDYCSSKGYNISWELGNEPNSFLKKADIFINGS 240
Db      181 GLDLIFGLNALIRTDADLQWNSNAQLLDYCSSKGYNISWELGNEPNSFLKKADIFINGS 240
Qy      241 QLGEDYIQLHKLRLKSTFKNAKLYGPDVGQPRRTAKMKLSFLKAGGEVIDSVTMHHYYL 300
Db      241 QLGEDYIQLHKLRLKSTFKNAKLYGPDVGQPRRTAKMKLSFLKAGGEVIDSVTMHHYYL 300
Qy      301 NGRTATREDPLNDVLDIFISSVQKVFQVVESTRGKKVWLGETSSAYGGAPLLSDTPA 360
Db      301 NGRTATREDPLNDVLDIFISSVQKVFQVVESTRGKKVWLGETSSAYGGAPLLSDTPA 360
Qy      361 AGFWMLDKLGLSARMGIEVVMRQVFEGAGNYHLVDENPDLDPDWLSLFLFKLVGTXYLM 420
Db      361 AGFWMLDKLGLSARMGIEVVMRQVFEGAGNYHLVDENPDLDPDWLSLFLFKLVGTXYLM 420
Qy      421 ASVQSSKRRKRLRVYLHCTNTDNPXYKEGDLTYAINTLHNTYKYLRLPYPSNKOVDKXYL 480
Db      421 ASVQSSKRRKRLRVYLHCTNTDNPXYKEGDLTYAINTLHNTYKYLRLPYPSNKOVDKXYL 480
Qy      481 RPLGPHGLSKSVQVNLGLTLKXVDDQTLPLMEKPLRPSSSLGLPAFSYSPFVIRAKYA 540
Db      481 RPLGPHGLSKSVQVNLGLTLKXVDDQTLPLMEKPLRPSSSLGLPAFSYSPFVIRAKYA 540
Qy      541 ACT 543
Db      541 ACT 543

RESULT 7
ADG88800
ID      ADG88800 standard; protein; 543 AA.
XX      AC      ADG88800;
XX      XX      11-MAR-2004 (first entry)
XX      DT      Human hpa protein.
XX      DE      Human hpa protein.
XX      KW      Wound healing; heparanase; ulcer; burn; laceration; surgical incision;
XX      KW      necrosis; pressure wound; diabetic ulcer; angiogenesis; human; therapy.
XX      OS      Homo sapiens.
XX      PN      US2003161823-A1.
XX      PD      28-AUG-2003.
XX      PF      14-JAN-2003; 2003US-00341582.
XX      PR      31-AUG-1998; 98WO-US017954.

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PR 01-MAY-1998; 98US-00071739.
 XX (INSI-) INSIGHT STRATEGY & MARKETING LTD.
 PA (HADA-) HADASIT MEDICAL RES SERVICES & DEV.
 PA (FRIE/) FRIEDMAN M M.
 XX
 PI Pecker I, Vlodavsky I, Friedman Y, Perets T;
 XX
 DR WPI; 2000-052944/04.
 DR N-PSDB; AA233290.
 XX
 PT Heparanase-specific molecular probes useful for diagnosis and treatment,
 PT e.g. of tumors, and for targeted drug delivery.
 XX
 PS Example; Page 81-82; 90pp; English.
 XX
 CC The present invention describes heparanase-specific molecular probes,
 CC useful for methods of detecting heparanase in situ. The probes and anti-
 CC heparanase antibodies are used to detect or quantify the expression of
 CC heparanase, for diagnosis and monitoring of diseases (especially
 CC metastasis), for treatment of heparanase-associated diseases (e.g.
 CC tumors), (adeno)carcinoma, squamous cell carcinoma, teratocarcinoma,
 CC mesothelioma, melanoma, lymphoma or leukemia, a solid cancer (or its
 CC metastases) derived from liver, prostate, bladder, breast, ovary, cervix,
 CC colon, skin, intestine, stomach, uterus and pancreas, kidney disease,
 CC diabetes and inflammation, haemorrhagic nephritis, nephrotic syndrome,
 CC sepsis and inflammatory or autoimmune disease), for targeted drug
 CC delivery (e.g. of anticancer agents) and as research reagents. The
 CC present sequence represents human heparanase, which is used in the
 CC exemplification of the present invention
 XX
 SQ Sequence 543 AA;
 Query Match 100.0%; Score 2842; DB 3; Length 543;
 Best Local Similarity 100.0%; Pred. No. 2.5e-273; Matches 543; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 541 ACI 543
 DB 541 ACI 543
 RESULT 5
 ID AA97635
 AA97635 standard; protein; 543 AA.
 XX
 AC AA97635;
 XX
 DT 20-APR-2001 (first entry)
 XX
 DE Human heparanase protein sequence.
 XX
 KW Heparanase; hnhp1; wound healing; angiogenesis; restenosis; Scrape;
 KW atherosclerosis; inflammation; pulmonary disease; Alzheimer's disease;
 KW neurodegenerative disease; Creutzfeldt-Jakob disease; viral infection;
 KW gene therapy; human.
 XX
 OS Homo sapiens.
 XX
 PN MO200100643-A2.
 XX
 PD 04-JAN-2001.
 XX
 PF 19-JUN-2000; 2000WO-IL000358.
 XX
 PR 25-JUN-1999; 99US-0140801P.
 XX
 PA (INSI-) INSIGHT STRATEGY & MARKETING LTD.
 XX
 PI Pecker I, Michael I, Itzhaki H;
 XX
 DR WPI; 2001-137930/14.
 XX
 PT New polynucleotides and polypeptides that are distantly homologous to
 PT heparanase, useful in wound healing, as well as in gene therapy protocols
 PT for angiogenesis, restenosis, atherosclerosis, or inflammation.
 XX
 PS Disclosure; Page 64-65; 67pp; English.
 XX
 CC This sequence represents a heparanase of the invention. The heparanase
 CC DNA and protein sequences are useful in wound healing, angiogenesis,
 CC restenosis, atherosclerosis, inflammation, pulmonary diseases,
 CC neurodegenerative diseases (such as Scrape, Alzheimer's disease, and
 CC Creutzfeldt-Jakob disease) or viral infections. The heparanase coding
 CC sequence is particularly useful in gene therapy
 XX
 SQ Sequence 543 AA;
 Query Match 100.0%; Score 2842; DB 4; Length 543;
 Best Local Similarity 100.0%; Pred. No. 2.5e-273; Matches 543; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 361 AGFMWLDKLGTSARMGIEVVMRQVFFGAGNYHLVDENPDLDPDYLSTLFFKLVGTXYLM 420
 DB 361 AGFMWLDKLGTSARMGIEVVMRQVFFGAGNYHLVDENPDLDPDYLSTLFFKLVGTXYLM 420
 QY 421 ASVQSKRRKRLRVYLHCTNTDNPVRYKESGDLTYAINLHVNTYKRLPYPFPSNKQVDKXYL 480
 DB 421 ASVQSKRRKRLRVYLHCTNTDNPVRYKESGDLTYAINLHVNTYKRLPYPFPSNKQVDKXYL 480
 QY 481 RPLGPHGLTSKSVQNLGLTLKMWDDOTLPPLMEKPLRPSSSLGLPAFSYFPIRANAKYA 540
 DB 481 RPLGPHGLTSKSVQNLGLTLKMWDDOTLPPLMEKPLRPSSSLGLPAFSYFPIRANAKYA 540
 QY 541 ACT 543
 DB 541 ACT 543

RESULT 3
 AAB08849
 ID AAB08849 standard; protein; 543 AA.
 AC AAB08849;
 DT 15-JAN-2001 (first entry)
 DE Amino acid sequence of a human heparanase polypeptide.
 XX Human; heparanase; gene therapy; tumour; inflammation; autoimmunity;
 KM heparin-binding growth factor; cytokine; neurodegenerative plaque;
 KM wound healing; infection; burn; angiogenesis; restenosis;
 KM atherosclerosis; inflammation; neurodegenerative disease;
 KM Gerstmann-Strausler Syndrome; Creutzfeldt-Jakob disease.
 OS Homo sapiens.
 XX WO200052178-A1.
 XX 08-SEP-2000.
 PD 14-FEB-2000; 2000WO-US003542.
 PF 01-MAR-1999; 99US-00258892.
 PR
 XX (INSI-) INSIGHT STRATEGY & MARKETING LTD.
 PA (HADA-) HADASIT MEDICAL RES SERVICES & DEV.
 PA (FRIE/) FRIEDMAN M M.
 PI Pecker I, Vlodevsky I, Feinstein E;
 DR MPI: 2000-579289/54.
 XX N-PSDB; AAA75051.
 XX
 PT New polynucleotides encoding a polypeptide having heparanase activity,
 PT useful in wound healing and in gene therapy, particularly in treating
 PT tumor, inflammation, autoimmunity, neurodegenerative diseases.
 XX
 XX Claim 22; Fig 1; 152pp; English.
 XX
 XX The present sequence represents a human protein with heparanase catalytic
 CC activity. The heparanase (hpa) polynucleotide is useful in gene therapy,
 CC particularly in treating tumour, inflammation or autoimmunity.
 CC Particularly, the polynucleotide is useful in modulating the
 CC bioavailability of heparin-binding growth factors, cellular responses to
 CC heparin-binding growth factors (e.g. bFGF) and cytokines (e.g.
 CC interleukin (IL)-8), cell interaction with plasma lipoproteins, cellular
 CC susceptibility to certain viral and some bacterial and protozoa
 CC infections, or disintegration of neurodegenerative plaques. The
 CC polynucleotide is also useful in wound healing (e.g. thermal, chemical or
 CC radiation burns), and in the treatment of angiogenesis, restenosis,
 CC atherosclerosis, inflammation, neurodegenerative diseases (Gerstmann-
 CC Strausler Syndrome or Creutzfeldt-Jakob disease), and some viral,
 CC bacterial or protozoa infections

XX SQ Sequence 543 AA;
 Query Match 100.0%; Score 2842; DB 3; Length 543;
 Best Local Similarity 100.0%; Pred. No. 2,56-273;
 Matches 543; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MLRSKRALPEPLMLLLGLPLSPGALPRPAQADVDVLDFTQEPHLHVSPLSVT 60
 DB 1 MLRSKRALPEPLMLLLGLPLSPGALPRPAQADVDVLDFTQEPHLHVSPLSVT 60
 QY 61 IDANLATPRFLILGLSPKRLTARGLSPAYLRFGGTDFLIPPKKESTEEBSYWS 120
 DB 61 IDANLATPRFLILGLSPKRLTARGLSPAYLRFGGTDFLIPPKKESTEEBSYWS 120
 QY 121 QVNODICKYGIIPDVEEKLREMPYOEOLLRHYOKKFKNSTYSSSDVLYTFANCS 180
 DB 121 QVNODICKYGIIPDVEEKLREMPYOEOLLRHYOKKFKNSTYSSSDVLYTFANCS 180
 QY 181 GDLIFGLNALRTADLQWSSNAQLLDYCSSKGYNISWELGNEBNSFLKKADIFINCS 240
 DB 181 GDLIFGLNALRTADLQWSSNAQLLDYCSSKGYNISWELGNEBNSFLKKADIFINCS 240
 QY 241 QLGEDYIQLHKLRLKSTFKNAKLYGPDVQPPRKTKAKMLKSLFKAGGEYIDSVTHHHYLL 300
 DB 241 QLGEDYIQLHKLRLKSTFKNAKLYGPDVQPPRKTKAKMLKSLFKAGGEYIDSVTHHHYLL 300
 QY 301 NGRTATREDPLNPVDLDFISSVOKVFOVVESTRPQKTYMLGETSSAYGGAPLISDTFA 360
 DB 301 NGRTATREDPLNPVDLDFISSVOKVFOVVESTRPQKTYMLGETSSAYGGAPLISDTFA 360
 QY 361 AGFMWLDKLGTSARMGIEVVMRQVFFGAGNYHLVDENPDLDPDYLSTLFFKLVGTXYLM 420
 DB 361 AGFMWLDKLGTSARMGIEVVMRQVFFGAGNYHLVDENPDLDPDYLSTLFFKLVGTXYLM 420
 QY 421 ASVQSKRRKRLRVYLHCTNTDNPVRYKESGDLTYAINLHVNTYKRLPYPFPSNKQVDKXYL 480
 DB 421 ASVQSKRRKRLRVYLHCTNTDNPVRYKESGDLTYAINLHVNTYKRLPYPFPSNKQVDKXYL 480
 QY 481 RPLGPHGLTSKSVQNLGLTLKMWDDOTLPPLMEKPLRPSSSLGLPAFSYFPIRANAKYA 540
 DB 481 RPLGPHGLTSKSVQNLGLTLKMWDDOTLPPLMEKPLRPSSSLGLPAFSYFPIRANAKYA 540
 QY 541 ACT 543
 DB 541 ACT 543

RESULT 4
 AAY52990
 ID AAY52990 standard; protein; 543 AA.
 AC AAY52990;
 DT 21-FEB-2000 (first entry)
 DE Human heparanase protein sequence.
 XX
 XX Human; heparanase; hpa; diagnosis; therapy; tumour; cyrostatic;
 KM antidiabetic; immunomodulatory; anti-inflammatory; nephrotropic;
 KM metastasis; adenocarcinoma; squamous cell carcinoma; teratocarcinoma;
 KM mesothelioma; melanoma; lymphoma; leukemia; cancer; sepsis; diabetes;
 KM inflammation; haemorrhagic nephritis; nephrotic syndrome;
 KM autoimmune disease; anticancer; kidney disease.
 OS Homo sapiens.
 XX
 XX WO9957153-A1.
 PD 11-NOV-1999.
 PF 29-APR-1999; 99WO-US009255.

CC conditions such as wound healing, angiogenesis, restenosis,
 CC atherosclerosis, inflammation, neurodegenerative diseases, and viral
 CC infections. Mammalian heparanase can be used to neutralize plasma
 CC heparin, and anti-heparanase antibodies may be applied for
 CC immunodetection and diagnosis of micrometastases, autoimmune lesions, and
 CC renal failure in biopsy specimens, plasma samples, and body fluids. The
 CC present sequence represents human heparanase

XX Sequence 543 AA;

Query Match 100.0%; Score 2842; DB 2; Length 543;

Best Local Similarity 100.0%; Pred. No. 2.5e-273; Mismatches 0; Indels 0; Gaps 0;

Matches 543; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLRSKPLPPMLLLGPIGLSPGALPRPAQADVDLDFTOEPHLVSPSLSYT 60
 DB 1 MLRSKPLPPMLLLGPIGLSPGALPRPAQADVDLDFTOEPHLVSPSLSYT 60
 QY 61 IDANLATDPRFLILGSPKRTLRAGLSPAYLRFQGTDFLIDPKKSTFEERSYQ 120
 DB 61 IDANLATDPRFLILGSPKRTLRAGLSPAYLRFQGTDFLIDPKKSTFEERSYQ 120
 QY 121 QVNODICKYGSIPDVVEKRLRLEMPYQEOQLLRHYQKFKNSTYSRSVDVLYTFANC 180
 DB 121 QVNODICKYGSIPDVVEKRLRLEMPYQEOQLLRHYQKFKNSTYSRSVDVLYTFANC 180
 QY 181 GDLIFGNALIRTDLQWNSNAQLLDYCSSKGYNISWELGNPNFLLKADIFINGS 240
 DB 181 GDLIFGNALIRTDLQWNSNAQLLDYCSSKGYNISWELGNPNFLLKADIFINGS 240
 QY 241 QUGEDYIQLHKLKLRSTFKNAKLYGPDVGQPRRTAKMLKSLKAGGEVIDSVTHHYYL 300
 DB 241 QUGEDYIQLHKLKLRSTFKNAKLYGPDVGQPRRTAKMLKSLKAGGEVIDSVTHHYYL 300
 QY 301 NGRATREDPLNPVDLDFISSVQKVFQVVESTRPGKXVWLGETSAYAGGAPLLSDTFA 360
 DB 301 NGRATREDPLNPVDLDFISSVQKVFQVVESTRPGKXVWLGETSAYAGGAPLLSDTFA 360
 QY 361 AGFMWLDKLGLSARWIEVVMQVFFGAGNYHLVDENFDPLDPYMLSLFKLVGKVLAM 420
 DB 361 AGFMWLDKLGLSARWIEVVMQVFFGAGNYHLVDENFDPLDPYMLSLFKLVGKVLAM 420
 QY 421 ASVQSKRRKRLRVYLHCTNTDNPRIYEGDLTYAINLNAVTKYLRLLPYPSNKKQVDKYL 480
 DB 421 ASVQSKRRKRLRVYLHCTNTDNPRIYEGDLTYAINLNAVTKYLRLLPYPSNKKQVDKYL 480
 QY 481 RPLGPHGLSKSVQNLGLTKXVDDOTLPLMEKPLRPSSSLGPRFSSFPVIRAKYA 540
 DB 481 RPLGPHGLSKSVQNLGLTKXVDDOTLPLMEKPLRPSSSLGPRFSSFPVIRAKYA 540
 QY 541 ACI 543
 DB 541 ACI 543

RESULT 2
 AA57590
 ID AA57590 standard; protein; 543 AA.

AC AA57590;

DT 02-MAR-2000 (first entry)

DE Human heparanase.

XX Human, heparanase; hpa; genetic modification; expression; anticancer;
 XX angiogenesis; anti-angiogenic; antiproliferative; antiviral; antitumor;
 XX anti-atherosclerotic; anti-inflammatory; antineurodegeneration;
 XX heparan sulphate; heparin-binding growth factor; tumour angiogenesis;
 XX metastasis; wound healing; restenosis; atherosclerosis; inflammation;
 XX neurodegeneration; viral infection; cystic fibrosis; cancer; diagnosis;
 XX micrometastasis; autoimmune lesion; kidney failure.

OS Homo sapiens.

XX WO957244-A1.

XX 11-NOV-1999.

XX 29-APR-1999; 99WO-US009256.

XX 01-MAY-1998; 98US-00071618.

XX 02-MAR-1999; 99US-00260038.

XX (INSI-) INSIGHT STRATEGY & MARKETING LTD.

XX (FRIE/) FRIEDMAN M.W.

XX Ben-Arzi H, Ayal-HersHKovitz M, Yacoby-Zeevi O, Pecker I;

XX Pelag Y, Shlomi Y;

XX WPI; 2000-062144/05.

XX N-PSDB; AA239195.

XX Engineered cells that express recombinant heparanase, useful

XX therapeutically, e.g. for treating angiogenesis and to screen for

XX specific inhibitors, potential anticancer agents.

XX Claim 3; Page 107-109; 118pp; English.

The present invention describes genetically modified cells (A) containing
 a polynucleotide (I) that encodes a polypeptide with heparanase activity,
 and express recombinant heparanase (II). Heparanase cleaves heparan
 sulphate (HS) at specific intrachain sites, resulting in release of
 heparin-binding growth factors, enzymes and proteins that are sequestered
 by HS in basement membranes, extracellular matrix or cell surfaces. It
 may also be implicated in tumour angiogenesis and metastases. (II) is
 potentially useful in wound healing and for treating angiogenesis,
 restenosis, atherosclerosis, inflammation, neurodegeneration, viral
 infection and cystic fibrosis. It can also be used to neutralise heparin
 (an alternative to protamine) and to screen for specific inhibitors
 (potentially useful for treating cancer and metastases). Antibodies
 raised against (II) are used for immunodetection and diagnosis of
 micrometastases, autoimmune lesions and kidney failure. (A) provide (II)
 in large quantities, in a form that is homogeneously processed and
 activated/neutralised by a dedicated protease. The present sequence
 represents human heparanase

XX Sequence 543 AA;

Query Match 100.0%; Score 2842; DB 3; Length 543;

Best Local Similarity 100.0%; Pred. No. 2.5e-273; Mismatches 0; Indels 0; Gaps 0;

Matches 543; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLRSKPLPPMLLLGPIGLSPGALPRPAQADVDLDFTOEPHLVSPSLSYT 60
 DB 1 MLRSKPLPPMLLLGPIGLSPGALPRPAQADVDLDFTOEPHLVSPSLSYT 60
 QY 61 IDANLATDPRFLILGSPKRTLRAGLSPAYLRFQGTDFLIDPKKSTFEERSYQ 120
 DB 61 IDANLATDPRFLILGSPKRTLRAGLSPAYLRFQGTDFLIDPKKSTFEERSYQ 120
 QY 121 QVNODICKYGSIPDVVEKRLRLEMPYQEOQLLRHYQKFKNSTYSRSVDVLYTFANC 180
 DB 121 QVNODICKYGSIPDVVEKRLRLEMPYQEOQLLRHYQKFKNSTYSRSVDVLYTFANC 180
 QY 181 GDLIFGNALIRTDLQWNSNAQLLDYCSSKGYNISWELGNPNFLLKADIFINGS 240
 DB 181 GDLIFGNALIRTDLQWNSNAQLLDYCSSKGYNISWELGNPNFLLKADIFINGS 240
 QY 241 QUGEDYIQLHKLKLRSTFKNAKLYGPDVGQPRRTAKMLKSLKAGGEVIDSVTHHYYL 300
 DB 241 QUGEDYIQLHKLKLRSTFKNAKLYGPDVGQPRRTAKMLKSLKAGGEVIDSVTHHYYL 300
 QY 301 NGRATREDPLNPVDLDFISSVQKVFQVVESTRPGKXVWLGETSAYAGGAPLLSDTFA 360
 DB 301 NGRATREDPLNPVDLDFISSVQKVFQVVESTRPGKXVWLGETSAYAGGAPLLSDTFA 360

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OM protein - protein search, using sw model

Run on: March 23, 2005, 11:09:57 ; Search time 113.5 Seconds
(without alignments)
1850.316 Million cell updates/sec

Title: SEQ2A
Perfect score: 2842
Sequence: 1 MLRSKPLPPLMLLGP.....LPFSYSPVIRNAKVAACI 543

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues
Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: _Geneseq_16Dec04:*
2: geneseqp19808:*
3: geneseqp19908:*
4: geneseqp20008:*
5: geneseqp20018:*
6: geneseqp20028:*
7: geneseqp20038:*
8: geneseqp20048:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	2842 100.0	543	2 AAY02345	Aay02345 A human h
2	2842 100.0	543	3 AAY57590	Aay57590 Human hep
3	2842 100.0	543	3 AAB08849	Aab08849 Amino aci
4	2842 100.0	543	3 AAY52990	Aay52990 Human hep
5	2842 100.0	543	4 AAY7635	Aay7635 Human hep
6	2842 100.0	543	5 ABB07813	Abb07813 Human hep
7	2842 100.0	543	7 ADG88800	Adg88800 Human hep
8	2842 100.0	543	7 ADL16379	Adl16379 Human hep
9	2842 100.0	543	8 ADMA8716	Adma8716 Human hpa
10	2842 100.0	592	2 AAY02346	Aay02346 A human h
11	2842 100.0	592	3 AAB08850	Aab08850 Amino aci
12	2842 100.0	592	7 ADG88804	Adg88804 Human SK-
13	2842 100.0	592	8 ADL16383	Adl16383 Human hep
14	2842 100.0	592	8 ADMA8720	Adma8720 Human SK-
15	2842 100.0	543	2 AAY17082	Aay17082 Human hep
16	2838 99.9	543	4 AAB86206	Aab86206 Human hep
17	2838 99.9	543	7 ADD18950	Add18950 Human dis
18	2838 99.9	543	8 ADK52086	Adk52086 Human ato
19	2838 99.9	543	8 ADMA8759	Adma8759 Human hpa
20	2838 99.9	543	8 ADNO5074	Adno5074 Antipsoi
21	2838 99.9	543	8 ADNO4902	Adno4902 Antipsoi
22	2838 99.9	543	8 ADQ80372	Adq80372 Hepatanas
23	2838 99.9	543	8 ADR88210	Adr88210 Human pre
24	2838 99.9	543	8 ADP25079	Adp25079 PRC Polyp
25	2838 99.9	588	2 AAY30124	Aay30124 A human p

26	2832	99.6	543	8 ADO63831	Ado63831 Human hep
27	2832	99.6	543	8 ADO63832	Ado63832 Human hep
28	2832	99.6	543	8 ADO63833	Ado63833 Human hep
29	2832	99.6	543	8 ADO63832	Ado63832 Human hep
30	2832	99.4	543	4 AAB88361	Aab88361 Human mem
31	2826	99.4	543	8 ADO63824	Ado63824 Human hep
32	2817	99.1	545	6 ABR56822	Abp56822 Human hep
33	2817	99.1	545	7 ADE16012	Adel6012 G-coupled
34	2817	99.1	545	8 ADL93951	Adl93951 Human G-c
35	2764	97.3	530	2 AAY34173	Aay34173 Human pre
36	2737	96.3	532	2 AAY17083	Aay17083 Seq ID No
37	2673.5	94.1	527	5 ABB07815	Abb07815 Chicken s
38	2673.5	94.1	527	7 ABR02018	Abv02018 Chimeric
39	2667.5	93.9	527	8 ADO63825	Ado63825 Chimeric
40	2667.5	93.9	527	8 ADO63826	Ado63826 Chimeric
41	2661.5	93.6	527	8 ADO63827	Ado63827 Chimeric
42	2146	75.5	535	3 AAR08851	Aar08851 A murine
43	2146	75.5	535	5 ABB07811	Abb07811 Mouse hep
44	2146	75.5	535	7 ADG88834	Adg88834 Mouse hpa
45	2146	75.5	535	8 ADL16413	Adl16413 Mouse hep

ALIGNMENTS

RESULT 1
AAY02345
ID AAY02345 standard; protein; 543 AA.

AC AAY02345;
DT 09-JUL-1999 (first entry)
XX
DE A human heparanase protein.

XX Heparanase; hp; modulator; heparin-binding growth factor;
XX cellular response; cytokine; cell interaction; plasma lipoprotein;
XX cellular susceptibility; infection; disintegration;
XX neurodegenerative plaque; wound healing; angiogenesis; restenosis;
XX atherosclerosis; inflammation; neurodegenerative disease; neutralise;
XX plasma heparin; micrometastasis; autoimmune lesion; renal failure.

XX Homo sapiens.
OS
XX
XX WO911798-A1.
XX
XX PN 11-MAR-1999.
XX
XX PF 31-AUG-1998; 98WO-US017954.
XX

XX 02-SEP-1997; 97US-00922170.
XX PR 02-JUL-1998; 98US-00109386.
XX

XX (INSI-) INSIGHT STRATEGY & MARKETING LTD.
XX (HADA-) HADASTIT MEDICAL RES SERVICES & DEV.
XX (FRIE/) FRIEDMAN M M.

XX Pecker I, Vlodavsky I, Feinstein E;
XX WPI, 1999-302255/25.
XX DR N-PSDB; AAX35648.
XX

PT New human polynucleotide useful for treating angiogenesis, restenosis,
PT and inflammation.

XX Claim 6, Fig 1, 63pp; English.

XX The specification describes a polypeptide having heparanase (hp)
XX activity. The recombinant protein is used as a modulator of heparin-
XX binding growth factors, cellular responses to heparin-binding growth
XX factors and cytokines, cell interaction with plasma lipoproteins,
XX cellular susceptibility to viral, protozoal and bacterial infections or
XX CC disintegration of neurodegenerative plaques. Heparanase may be useful for

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QY 106 PKKESTFEERSYQWQVNOQDICKYGSIPDVEBKRLIEMPYOQLLREHYOKKFKFNSTY 165
DB 100 -SKENI-----PISCHNCYSKSPKSLCO--LIEKPC-----KHKKFLPFLIM 140
QY 166 SSSSVADVLTTPANCGLDILIFGLNALLRTRADLOWNSNAQLLIDYSSSGYNI SWELGNE 225
DB 141 TQENENQIJDPCRKTMLKLLFSLNAMLRD--NIGWNNKNARELIEFKHQVYADWQLGNE 199
QY 226 PMSFLKKADIFINGSLGEDIYQLHKLRLKSTFPKNAKLYGPDVGOP---RRKTAKMLKSF 282
DB 200 PMSFGHVENESTYPOQLADQFEKRLKRLNHNNGRSHLIVGPDTPTRQPRPELKTMIFF 259
QY 283 LKAGGEVIDSVTMHHYILNGRTATREDPLNPVLDLIFISSVOKPFOVESTPCKKY--W 340
DB 260 LQNGSHYIVNRSWHQYILNSKTAKLEDFNWPEFFDL---RQILEMQQTKYKXNI PMW 316
QY 341 LGETSAYGGGAPLSDTPAAGFMWLDKLGSAKMGIEVVMQVFFGAAGNYHLVDENPDP 400
DB 317 LSETSSYGGGAPGLSNTYAGSPLMIDKLGLSAKYNI STVIRQSFIG--GYSSLVDENLKP 375
QY 401 LFDYMLSLFPKLVGKVLMAVQGSKRRLRYVLAHTNTDNPRYKE--GDLLTYAIN-- 456
DB 376 LFDWMISLVYKLVGNKVL--QVQNCSTPFRQRYLHCTNR--KYNDTSAYTLVGVNLE 430
QY 457 -----LHN-----VTXYLRLLPYPSNKOVDKYLRLPLGPHGLSKSVQNLGLTL 500
DB 431 MAKARFPLNGTALHGDDLIHEXYI--ISAPSNRK-----SKTLLNGWPL 474
QY 501 KNAVDDOTLPPIMEKPLRPGSSSLGAPAFSYSPFYTRAKYAAAC 542
DB 475 YV--ESNLHNLRPNIHRYGRVYSLPPYSIGFWIKKTSITVC 514

RESULT 15
Q9SDAI PRELIMINARY; PRT; 521 AA.
AC Q9SDAI;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, last annotation update)
DE Hypothetical protein F13G24.30.
GN Name=F13G24.30.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosid II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxId=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA Bevan M., Van Der Schueren J., Chuang Y.J., Voet M., Robben J.,
RA Volckaert G., Bancroft I., Mewes H.W., Lemcke K., Mayer K.F.X.;
RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA EU Arabidopsis sequencing project;
RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL133421; CAB62595.1; -.
DR PIR; T45608; T45608.
DR InterPro; IPR005199; Glyco_hydro_79N.
DR InterPro; IPR001254; Peptidase_S1.
DR Pfam; PF03662; Glyco_hydro_79n; 1.
DR PROSITE; PS00135; TRYPSIN_SER; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 521 AA; 57831 MW; 07D864A4B305CC2 CRC64;

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Query Match 14.6%; Score 416; DB 2; Length 521;
Best Local Similarity 29.2%; Pred. No. 1.6e-22;
Matches 154; Conservative 68; Mismatches 184; Indels 122; Gaps 24;

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```

QY 75 LGSPEKRLTARGSPAYLRFQGTIKTDFLFDPKKESTFEERSYQWQVNOQDICKYGSIPP 134
DB 55 LTRPPLLTAKAKPKPLRIRIGSLQDOVIYDGNLKT-----PCR----- 94

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QY 135 DVEBKRLIEMPYOQLLREHYOKKFKNS--TYSRSSV-----DLYTTPANCGLDILF 186
DB 95 -----PQOKM-----NSGLRGFSKGLCHMRKMDLNLFLATGAVTF 132
QY 187 GLNALIRTDLQ-----WNSNNAQLLIDYSSSGYNI--SWELGNEPMSFLKKADIFIN 238
DB 133 GLNALIRGRHKLKRGKAMGAMDHINQDFLNTYVSKGYVIDSWFEGNELSG--SGVASVS 190
QY 239 GSQLEDYIQLHKLRLKSTFPKNAKLYGPDVGOP---RRKTAKMLKSFLLKAGGEVIDSV 293
DB 191 AELYGKDLIVLQDVINK--VYKNSMLHKPLIVAPGGFYEQGWYTKLLET---SGPSVVDV 246
QY 294 TWHHYILNGRT--ATREDFLNPVDLIDFISVQKVF---QVESTPCKKYWLGETSSA 347
DB 247 THHIVYLGSGNDPALVKKIMDPS---YLSQVSKTFKDVNQTIQEHGPWASPVGESGA 302
QY 348 YGGGAPLSDTPAAGFMWLDKLGSAKMGIEVVMQVFFGAAGNYHLVD--NPDPLDYVL 406
DB 303 YNSGGRHVSDFITDSFWYLDOLGMSARHNTKYCRQTLVG--GFYGLLEKGTVPNPDDYS 361
QY 407 SLFPKLVGKVLMAVQGSKRRLRYVLAHTNTDNPRYKEGDLTYAINTLHNTKYL-- 464
DB 362 ALIMHRLMKGVLAVQTDGPP--QLRVYAHCK-----GRAGVTLLINLSQSGDFYVS 413
QY 465 -----RLPYPS---NKQVDKYLRL--LGPHG--LISKSVDL 495
DB 414 VSNGINVVLNAESRKKKSLDLTLKRPFSWIGSKASDPGYNLRBYHLTPENGVLRSKTMVL 473
QY 496 NGTILTKMVDOTLPPIMEKPLRP--GSSSLGAPAFSYSPFYTRAKYAAAC 542
DB 474 NGRSLKPTATGDI PSL--EPVLSVNSPLNVLPLMSFIVLPNPDASAC 520

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Search completed: March 23, 2005, 11:29:33
 Job time : 112.5 secs

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Db 78 FLSTLDPSIIHD-CMLDPLSKRLVTLARGSPFLRFGKRTPLQONLRNPKSRG 136
Qy 112 FEERSYWGQVNOQDI-----CKYGSIPRVEEKLRLRLEMPYQOL-LLRHHYK 158
Db 137 GGGPRTYLNKYRDDIIVRSVDALDKQKCKIAQ-HEDVMELQREKRAQHMLVLEQF-- 193
Qy 159 KFKNSTYKSSVDVLYTFPANCGLDLIFGLNALRLTADLQWSSNAQLLLDYCSSKGYNI 218
Db 194 ---SNTYS-----NIL-----202
Qy 219 SWELGNEPNSFLKADIFINGSQLEDYIQLHKLKR-STFKNAKLYGPDVQPRRTAK 277
Db 203 -----TEPNRYRTMGRAVNGSOLGKDYIQLKSLQPIRIRYRASLYGNIRPRKAVIA 257
Qy 278 MLKSPFKAGGEVYIDSVTHHHYLLNGRTAREDFLNPVDLIFISSVQKQFQVYESTRPRK 337
Db 258 LLDGFMKAVASTVDATWQHCTIYDGRVVKWMPFLKRLDLTSDQIRKIQKVVNTYTPGK 317
Qy 338 KVMLETSAYGGAPLSDTFAAGFMWLDKLSARMGIEVVMQVFPFAGNHYLVNEN 397
Db 318 KIMLSGVVTSAGGNNISDSYAGFLMLNTLGLMLANGIDVIRHSFDDHGYNHLVDQN 377
Qy 338 FPLPDYVWLSLFLKVLGTVKYLMAVQSKRR-----KLRYLHCTNTDNPYKEG 448
Db 378 FNPPLDYWLSLFLKVLGTVKYLMAVQSKRRPGRVIRDKLRIYACHTNNHNNHYVAG 437
Qy 449 DLTVAINHANTYKYLRLPYPSNKQVNDKYLRLPGPHGLSKSVOLNGLTKWDDOTL 508
Db 438 SILLTINLHRSRKKIKLAGTRDKLVHGYLLQPGQGLSKSVOLNGLTKWDDOTL 497
Qy 509 PLMEKPLRPGSSGLPAPSVSFVIRNAKVAAC 542
Db 498 PELKRPRLRAGRTLVIPVTMGFPFVKNVNALAC 531

RESULT 13
Q9HB39 PRELIMINARY; PRT; 480 AA.
ID Q9HB39;
AC Q9HB39;
DT 01-MAR-2001 (Tremblrel. 16, Created)
DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)
DT 01-MAR-2004 (Tremblrel. 26, Last annotation update)
DE Heparanase-like protein HPpaz.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OC NCBI_TaxId=9606;
RN (1)
RP SEQUENCE FROM N.A.
RX MEDLINE=20483645; PubMed=11027606; DOI=10.1006/dbrc.2000.3586;
RA McKenzie E., Tyson K., Stamps A., Smith P., Turner P., Barry R.,
RA Hirock M., Patel S., Barry E., Stuberfeld C., Terrett J., Page M.;
RT "Cloning and expression profiling of Hpa2, a novel mammalian
RT heparanase family member.";
RL Biochem. Biophys. Res. Commun. 276:1170-1177 (2000).
RN (2)
RP SEQUENCE FROM N.A.
RA McKenzie E.A., Tyson K., Stamps A.;
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF282885; AAG23421.1; -.
DR PIR; JC7506; JC7506.
DR InterPro; IPR005199; Glyco_hydro_79N.
DR Pfam; PF03662; Glyco_hydro_79n; I.
SQ SEQUENCE 480 AA; 53900 MW; F75F8967AC1F83 CRC64;

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Query Match 31.6%; Score 897.5; DB 2; Length 480;
Best Local Similarity 36.0%; Pred. No. 9, 4e-59;
Matches 202; Conservative 74; Mismatches 146; Indels 139; Gaps 9;

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Qy 20 PLGLSPAL-----PRPA-----QAQVVDLDFTOEPFLHVS 55
Db 18 PPACIAPGALYLLALHLSLSSQAGDRRLPVDRAAGLKEKTLILDVSTKNPRTVNMEN 77

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Qy 56 FLSTIDANLATDPRFLLILGSPKLTTLARGSPAYLRFGTGTDPLIF----DPKEST 111
Db 78 FLSTLDPSIIHD-CMLDPLSKRLVTLARGSPFLRFGKRTPLQONLRNPKSRG 135
Qy 112 FEERSYWGQVNOQDICKYGSIPRVEEKLRLRLEMPYQOLLLREHYOKFKNSTYRSSVD 171
Db 136 -----GGPDP-----YLYKNYE-----148
Qy 172 VLYTFPANCGLDLIFGLNALRLTADLQWSSNAQLLLDYCSSKGYNISWELGNEPNSFLK 231
Db 149 -----DEPNRYRT-----156
Qy 222 KADIFINGSQLEDYIQLHKLKR-STFKNAKLYGPDVQPRRTAKMLKSPFKAGGEVY 290
Db 157 MHGRAVNGSOLQKDYIQLKSLQPIRIRYRASLYGNIRPRKAVIALLDGFMKAVASTV 216
Qy 231 DSVTHHHYLLNGRTAREDFLNPVDLIFISSVQKQFQVYESTRPRKVMLETSAYG 350
Db 217 DAVTWQHCHYIDGRVVKWMPFLKRLDLTSDQIRKIQKVVNTYTPGKIMLEGVNTSAG 276
Qy 351 GAPILSDTFAAGFMWLDKLSARMGIEVVMQVFPFAGNHYLVNENPDLPDYVWLSLFL 410
Db 277 GTNNISDSYAGFLMLNTLGLMLANGIDVIRHSFDDHGYNHLVDQNFNPLPDYVWLSLY 336
Qy 411 KVLGTVKYLMAVQSKRR-----KLRYLHCTNTDNPYKEGDLTYAINHANTY 461
Db 337 KRLIPKTLAVHAGLQKRRPGRVIRDKLRIYACHTNNHNNHYVAGSITLFIINLHRSR 396
Qy 462 KYLRLPYPSNKQVNDKYLRLPGPHGLSKSVOLNGLTKWDDOTLPLMEKPLRPGSS 521
Db 397 KKIKLAGTRDKLVHGYLLQPGQGLSKSVOLNGLTKWDDOTLPELKRPLRAGRT 456
Qy 522 LGLPAPSVSFVIRNAKVAAC 542
Db 457 LVIPVTMGFPFVKNVNALAC 477

RESULT 14
Q8T108 PRELIMINARY; PRT; 515 AA.
ID Q8T108;
AC Q8T108;
DT 01-JUN-2002 (Tremblrel. 21, Created)
DT 01-JUN-2002 (Tremblrel. 21, Last sequence update)
DT 05-JUL-2004 (Tremblrel. 27, Last annotation update)
DE Heparanase-like protein.
OC Eukaryota; Metazoa; Chordata; Hexapoda; Insecta; Pterygota;
OC Bombyx mori (Silk moth).
OC Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Bombycoidea;
OC Bombycidae; Bombyx.
OC NCBI_TaxId=7091;
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN=PS0; TISSUE=Posterior silkgland;
RA Koike Y., Mita K., Suzuki M.G., Maeda S., Abe H., Osoegawa K.,
RA deJong P.J., Shimada T.;
RT "Genomic sequence of a 320-kb segment of the Z chromosome of Bombyx
RT mori containing a kettin ortholog.";
RL Mol. Genet. Genomics 269:137-149 (2003).
DR EMBL; AB079860; BAB85191.1; -.
DR EMBL; AB090307; BAC10612.1; -.
DR InterPro; IPR005199; Glyco_hydro_79N.
DR Pfam; PF03662; Glyco_hydro_79n; I.
SQ SEQUENCE 515 AA; 59769 MW; FB8100AB6EDDADB CRC64;

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Query Match 24.5%; Score 696; DB 2; Length 515;
Best Local Similarity 35.1%; Pred. No. 1, 4e-43;
Matches 183; Conservative 83; Mismatches 182; Indels 74; Gaps 18;

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```

Qy 46 QEPHLVSPFLSTIDANLATDPRFLLILGSPKLTTLARGSPAYLRFGTGTDPLIF 105
Db 42 QEDIKLISEDFLSRID-TIEIENYNRINYSDBTLRLRLAALSPARLRLGGTMSERLIF- 99

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QY 20 PLGLPSGAL-----PRPA-----QAQDVVDLDFPTQEPHLVSPS 55
| : : : : :
DB 18 PACACLAGALYALALLHLSSQAGDRRLPVDRAAGLKEKTLILLDVSTKPVRTVNEV 77
| : : : : :
QY 56 FLSTVITDANLADPPRLILLGSPKRTLRAGSPAYLRFGGKTDPDLF---DPKKEST 111
| : : : : :
DB 78 FLSTLDPSIIHD-GWLDPLSSKRLVTLARGLSPAFLRGGRKTFLOQNLINPAKSRG 136
| : : : : :
QY 112 PEERSYQSQVQVNDI-----CKYGSIPRVEEKLRLWEPYEQQL-LIREHYOK 158
| : : : : :
DB 137 GGGPRTYLYKNYEDDVIYRSVDALDKQKCKIAQ-HPDVMELOREKRAQNHVLLKEQFEN 195
| : : : : :
QY 159 KFKNSTYSSSVYDVIYTFPANCGLDLIFGNALRLTADLQWNSNAOLLDDYCSSKXNYI 218
| : : : : :
DB 196 TVSNILILTRSLDKLYNSADCSGLHLIFALNLRPNNSMSSSLKTKYSASKKXNYI 255
| : : : : :
QY 219 SWELGNEPNPSFLKADIFINGSOLGSDYIQLHKLRLK-STFKNAKLYGSDVQPRKRTAK 277
| : : : : :
DB 256 SWELGNEPNPNYRTMHGRAVNGSQLGQDYIQLKSLQPIRTYSRASYGNIRPRKNVIA 315
| : : : : :
QY 278 MKSFLKAGGEVIDSTWHYLYNGRTATREDPLNDVDLDFISSVQKFOVVESTRPGK 337
| : : : : :
DB 316 LLDGFMKAVGSTVDATWQHCYIDGRVVKVMDPLKTRLLDITLSDQIRKIQKVVNTYTPGK 375
| : : : : :
QY 338 KVMLGFTSSAYGGAPRLSDTPAAGFMWLDKGLSARMGIEVVMRQVFFGAGNYHLVDEN 397
| : : : : :
DB 376 KTWLEGVVTTAGGTNNLSDSYAAGFLMNTLGMLANOGIDVYIRHSFDDHGNHLVDQN 435
| : : : : :
QY 398 FPPPLPYWLSLFLKLVGTKVLMASVQSKRR-----KLRYVLHCTNTDNPKYKKG 448
| : : : : :
DB 436 FNPPLPYWLSLFLKLVGTKVLMASVQSKRR-----KLRYVLHCTNTDNPKYKKG 495
| : : : : :
QY 449 DTLVYINLHNTKYLRPYPFENKQVDKYLRLPGLPHGLSKSVOLNGLTLMVDDQTL 508
| : : : : :
DB 496 SITLPLIINHRSRKKIKLAGTLRDKLVHGYLLQPYQGBGLKSKSVOLNGOLPLMVDDGTL 555
| : : : : :
QY 509 PPLMEKPLRPGSSGLPAFYSFFVIRNAKVAAC 542
| : : : : :
DB 556 PELKPRPLRAGRTLVPVTMGFFVKNVNALAC 589
| : : : : :

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RESULT 11
Q9WMQ1 PRELIMINARY; PRT; 548 AA.
AC Q9WMQ1;
DT 01-MAR-2002 (TREMBlrel. 20, Created)
DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE Heparanase 3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Prostate;
RA Legoux P., Legoux R., O'Brien D., Salome M.;
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Prostate;
RA Pessague Saotomas B.U.O.P.S.;
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ299720; CAC82492.1; -
DR Pfam; PF03662; Glyco_hydro_79n; 1.
SQ SEQUENCE 548 AA; 61771 MW; B8986303FC73A60A CRC64;

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Query Match 35.7%; Score 1015.5; DB 2; Length 548;
Best Local Similarity 41.8%; Pred. No. 1.6e-67;
Matches 224; Conservative 79; Mismatches 180; Indels 53; Gaps 9;
QY 8 ALPPLMLLGLGLPSGAL-----PRPA-----QAQDVVDLDF 43
| : : : : :

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DB 6 AFPEAMLSNSRPPACLAGALYALALLHLSSQAGDRRLPVDRAAGLKEKTLILLDV 65
| : : : : :
QY 44 FTOEPLHVSBSFLSVITDANLADPPRLILLGSPKRTLRAGSPAYLRFGGKTDPDLI 103
| : : : : :
DB 66 STKNVVRVYVNEFSLQDPSIIHD-GWLDPLSSKRLVTLARGLSPAFLRGGRKTFLO 124
| : : : : :
QY 104 F---DPKKESTFEERSYQSQVQVNDI-----CKYGSIPRVEEKLRLWEPYEQ 147
| : : : : :
DB 125 FQNLINPAKSRGPGPDYLYKNYEDDVIYRSVDALDKQKCKIAQ-HPDVMELOREKQAQ 183
| : : : : :
QY 148 EQL-LIREHYOKKFKNSTYSSSVYDVIYTFPANCGLDLIFGNALRLTADLQWNSNAQL 206
| : : : : :
DB 194 MHLVLLKQFQSVNTYNNLILTRASLDKLYNSADCSGLHLIFALNLRPNNSMSSSLAS 243
| : : : : :
QY 207 LLDYCSSKXNYISWELGNEPNPSFLKADIFINGSOLGSDYIQLHKLRLK-STFKNAKLYG 265
| : : : : :
DB 244 LKYSASAKKXNYISWELGNEPNPNYRTMHGRAVNGSQLGQDYIQLKSLQPIRTYSRASYG 303
| : : : : :
QY 266 PIVGQPRKRTAKMLKSFKAGGEVIDSTWHYLYNGRTATREDPLNDVDLDFISSVQK 325
| : : : : :
DB 304 PNIGRPRKNVIALLDGFMKAVGSTVDATWQHCYIDGRVVKVMDPLKTRLLDITLSDQIRK 363
| : : : : :
QY 326 VQOVVESTRPGKVMLGFTSSAYGGAPRLSDTPAAGFMWLDKGLSARMGIEVVMRQVF 385
| : : : : :
DB 364 IOKVVNTYTPGKKTWLEGVVTTAGGTNNLSDSYAAGFLMNTLGMLANOGIDVYIRHSF 423
| : : : : :
QY 386 FGAGNYHLVDENFDPDYWLSLFLKLVGTKVLMASVQSKRR-----KLRYVLH 436
| : : : : :
DB 424 FPHGNYHLVDQNFNPLPDYWLSLFLKLVGTKVLMASVQSKRR-----KLRYVLH 483
| : : : : :
QY 437 CTNTDNPKYKKGDTLVLAINLHNTKYLRPYPFENKQVDKYLRLPGLPHGLSKSVOLNGLT 492
| : : : : :
DB 484 CTNHNNHNVYRGSITLFIINLHRSRKKIKLAGTLRDKLVHGYLLQPYQGBGLKSKT 539
| : : : : :

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RESULT 12
Q9HB38 PRELIMINARY; PRT; 534 AA.
AC Q9HB38;
DT 01-MAR-2001 (TREMBlrel. 16, Created)
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE Heparanase-like protein HP42b.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20483645; PubMed=11027606; DOI=10.1006/dbrc.2000.3586;
RA McKenzie E., Tyson K., Stamps A., Smith P., Turner P., Barry R.,
RA Hircok M., Patel S., Barry E., Stuberfield C., Terrett J., Page M.;
RT "Cloning and expression profiling of Hpa2, a novel mammalian
heparanase family member";
RL Biochem. Biophys. Res. Commun. 276:1170-1177(2000).
RN [2]
RP SEQUENCE FROM N.A.
RA McKenzie E.A., Tyson K., Stamps A.;
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF282886; AAC23422.1; -
DR InterPro; IPR005199; Glyco_hydro_79n.
DR Pfam; PF03662; Glyco_hydro_79n; 1.
SQ SEQUENCE 534 AA; 60063 MW; C3DE5E90C8338C4 CRC64;

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Query Match 33.0%; Score 936.5; DB 2; Length 534;
Best Local Similarity 37.8%; Pred. No. 1.3e-61;
Matches 217; Conservative 78; Mismatches 168; Indels 111; Gaps 12;
QY 20 PLGLPSGAL-----PRPA-----QAQDVVDLDFPTQEPHLVSPS 55
| : : : : :
DB 18 PACACLAGALYALALLHLSSQAGDRRLPVDRAAGLKEKTLILLDVSTKPVRTVNEV 77
| : : : : :
QY 56 FLSTVITDANLADPPRLILLGSPKRTLRAGSPAYLRFGGKTDPDLF---DPKKEST 111
| : : : : :

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	Matches	320;	Conservative	87;	Mismatches	114;	Indels	11;	Gaps	3
Qy	13	LMLLLLPGLGSLSGALPRPAOADVDDLEFTFOEPHLVSPFSLSVTIDANLADPPRL	72							
Dd	2	LVLLLLLVLLAVPP-----RTTALDGLGRPEIDAVPAPFLSTLDASLADPPRFV	52							
Qy	73	ILGSPKLRTLARGLSPAYLARFGGKTDPFLIFDPKESTFEERSYWGOSQVNDICKYSI	132							
Dd	53	ALLRHPKLHTLASGLSPOGLRFGGTSDPFLFNPKKDSITWEKKYLSEFQA-KDVEANPS	111							
Qy	133	PPDVEEKLRLMPYOEOULLREHYOKPKNSITYSSRSVDVIYTFANCSGDLDFIGLANLL	192							
Dd	112	FAVPKLLLTQWPIQEKLILLAEHSWKKGKNTTTIRSTLDIHTFASSGGFRVLFGIANLL	171							
Qy	193	RTADLONNSSNAOULLDWCSCKNYISMEIGNENPMSPLAKDAIFINGSQLGEDTYQLAKL	252							
Dd	172	RRAGLDOWSSNAKOLLGYCAQRSNYISMEIGNENPMSFKKSGCICIDGFOLGDPFHNLQL	231							
Qy	253	L-RKSTKPMNALKYPDYGOQPRRKTAOMLKFELKAGEVIDSYTWTHYYLNGSTRATEDPL	311							
Dd	232	LSQHPLRHAEYLGLDVQGPKRKHQHLIRSTMKSCKAIDSWTWHYYVNGSAIRDEPL	291							
Qy	312	NPDVLDIFFISSVOXVPQVESTRPCKKYWLGETSSAYGGAPLSDTPAAGFMWLDKGL	371							
Dd	292	SPEVLDSFPATLIHDVTLGIVEATVDEGKKWMLGETSGAYGGAPQLSNTFYAGFMWLDKGL	351							
Qy	372	SABWGIEVMWQVFEGAGNYHLVDENPPLDWDYSLLFKKLYGKYLMAVSOGSKRRKL	431							
Dd	352	AARGCIDVMWQVSEFAGSYHLVDGEFPLPYMWISTLYKRYLGTRVLAQASEQADARRP	411							
Qy	432	RVLVLCNTDNRKYEGDDLTYAINLNVTXYRLRPFYPSNKQVDKYLLRPVPGHLSLK	491							
Dd	412	RVYLHCINPRHPKYREGDVTLPALNLSNVTSIQPKQLWSKSVQYIYLLPHGXDSILSR	471							
Qy	492	SVQANGLTLLKAVDDQDTLPRLMEKPLRPSSSIGLPAFSISFPIYIRAKYAACI	543							
Dd	472	EVOJNGRLLOWVDETLPALHEMALAPGSTGLPAFSGFYAIRAKAIACI	523							
<hr/>										
RESULT 9										
ID	Q9HB37	PRELIMINARY:						PRT:	592 AA.	
AC	Q9HB37,									
DT	01-MAR-2001 (TREMBLrel. 16; Created)									
DR	01-MAR-2001 (TREMBLrel. 16; Last sequence update)									
DT	01-JUN-2003 (TREMBLrel. 24; Last annotation update)									
DE	Heparanase-like protein HPAZC.									
OS	Homo sapiens (Human).									
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;									
CC	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.									
OX	NCBI_TaxId=9606;									
RN	[1]									
RP	SEQUENCE FROM N.A.									
RX	MEBLINE=20483645; PubMed=11027606; DOI=10.1006/bdrc.2000.3586;									
RA	McKenzie B., Tyson K., Stamps A., Smith P., Turner P., Barry R.,									
RL	Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.									
DR	EMBL; AF282887; AAC3423.1; "									
GO	GO:0005622; C:intracellular; TAS.									
DR	GO:0003035; F:heparanase activity; TAS.									
DR	InterPro: IPR005199; Glyco_hydro_79N.									
DR	pfam; PF03662; Glyco_hydro_79n; I	</								

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QY 20 PLGJLSGAL-----PRPA-----QAQVDVLDPEFTEPHLVSBS 55
Db 18 PRCLAAGALYALLLHLSLSSQAGDRPLPVDPAAGKAKETILLIDYSTKNPATVVEN 77
QY 56 FLAVTIDANLATDPRFILLGSPKRLTARGLSAPYLRFGGKTDFLIF---DPEKST 111
Db 78 FLISQIDPISIIHD-GWIDFLSSKRLLVTLARGLSAPFLRFGGKRDFDQFOLIRNPANRSG 136
QY 112 PEERSYQOSQOVNODI-----CKYSSIPPDVEBKRLRMPYEOUL-LREHYOK 158
Db 137 GPGGDYLLKNUVEDIVRSVDALDKQKGCKLAQ-HPDWALRLQREKQAMHLYLKEQFSN 195
QY 159 KFKRSTYSRSRSDVLYTTPANCGLDIFGLNALRTADLOKNSSNAQOLLDYCSSKGNV 218
Db 196 TYSNLIITANSBDKLYINPADSCGHLFLALNALRPNPNNSWNSSALSILKYSASKKTVI 255
QY 219 SWEIGNEPNSFLKKADIFINGSQUGEDYIQLHLKR-STFKNALKYGPVGOAPRKATAK 277
Db 256 SWEIGNEPNRYRTMHRGAUVNSQUGKOYLOKSLLOPIRISBSLYGPNIKGRPKNVIA 315
QY 278 MLKSFLLKAGEVIDSVTHNYTLNGRTRATREDFLNPVDVLI-FISSQVKVFOVVESTREK 337
Db 316 LLGDFMFLVASTVDVAVWOHCYIDGRVVKVMDFLKTRLLDLSQIRIKOKVNVYTRGK 375
QY 338 KVMJGETSSAYCGGAPLLSDTFPAAGFMWLDLGLSABKIGEVNWRQVEFAGNVHLDVEN 397
Db 376 KIMLEGVYTTISAGGTNNLSDSYAAGFMLNLTLGMLANOIGIDIVYLRHSFDDHGYNHLVDON 435
QY 398 FDPFLPDYWLSLFFKFLVGTKVLMASVQSSKKR-----KLRYVLTCTWTDNRYREG 448
Db 436 FNPFLPDYWLSLYKRLIGPKVLAHVAGLOQKKRPRGARVIRKRLRYANCTNNHNNHYVRG 495
QY 449 DLTLYAINLHNVTKYLRLEYPESKKQVDKYLRLPLRPHGLLSQVQLNGLTLKAYDDOTL 508
Db 496 SITFLFINLHRSRRKIKLAGTRKLVHQYLLQYLOGEQGLKSSQVQLNGQPLWVDGTL 555
QY 509 PLMEKRLRQSSSGLPAFSYFSEVINAKYAAAC 542
Db 556 PELKRPRLRAGRTLVIPVTVGWFFVVKVNALAAC 589

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RESULT 10
08WMQ2
ID 08WMQ2 PRELIMINARY; PRT: 592 AA.
AC 08WMQ2;
DT 01-MAR-2002 (TReMBLrel. 20, Created)
DT 01-MAR-2002 (TReMBLrel. 20, last sequence update)
DT 01-MAR-2003 (TReMBLrel. 23, last annotation update)
DE Heparinasae 2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Prostate;
RA Legoux P., Legoux R., O'Brien D., Salome M.;
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Prostate;
RA Pessague Safontas B.J.O.P.S.;
RL Submitted (SRP-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ299719; CAC82491.1; -.
DR Genew; HGNC:18374; HPSE2.
DR Pfam; PF03662; Glyco_hydro_79n; 1.
SQ SEQUENCE 592 AA; 66520 MW; 9478841FEACD558B CRC64;

Query Match 40.3%; Score 1146.5; DB 2; Length 592;
Best Local Similarity 43.4%; Pred. No. 2.5e-77;
Matches 249; Conservative 82; Mismatches 190; Indels 53; Gaps 9

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RP SEQUENCE FROM N.A.
RA Hulest M.D., Wang J., Hornby J.R., Freeman C., Pagler E., McHenry J.,
RA Parish C.R.;
RA Submitted (Mar-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF359508; AA015189.1;
DR InterPro: IPR005199; Glyco_hydro_79N.
DR Pfam: PF03662; Glyco_hydro_79n; 1.
SQ SEQUENCE 536 AA; 60479 MW; C434E04CF536EA4D CRC64;
Query Match 75.1%; Score 2135; DB 2; Length 536;
Best Local Similarity 76.1%; Pred. No. 1.2e-151;
Matches 407; Conservative 50; Mismatches 78; Indels 0; Gaps 0;
QY 9 LPPMLLLGLPGLSPGALPPAQAQDVVDLDFPQEPHLVSPSPSLVTIDANLATD 68
DB 2 LRPLLLMKRLALVGTGTAAGTAPTKVDVLDLFTYKRLFGQSPSPSLSTIDASLATD 61
QY 69 PRFLILGSPKRLTLARGSPAYLRFGGKTDFLIPPKKESTFEERSYWGQVQNDICK 128
DB 62 PRFLTLGSPRLRLARGSPAYLRFGGKTDFLIPPKKESTFEERSYWGQVQNDICK 121
QY 129 YGSIIPDVEKRLLEMPYQOQLLRHNYQKKFKNSTYSSSDVLYTFANSGDLIFGL 188
DB 122 SERVSADVLRKIQEMWPFQELLLREOYQREPKNSTYSSSDVLYTFANSGDLIFGL 181
QY 189 NALLRTADLQNNSSNAQQLLDYCSSKGYNISWELGNEPNSFLKKADIFINGSOLGEDYIQ 248
DB 182 NALLRTADLQNNSSNAQQLLDYCSSKGYNISWELGNEPNSFLKKADIFINGSOLGEDYIQ 241
QY 249 LHKLLRKSTFKNAKLYGPDVQPRRKTAQMLKSLFKAGEVIDSVTWHYYLNGRTATRE 308
DB 242 LHKLLQKSAFQNAKLYGPDIGQPRGKTIVKLRSFLKAGEVIDSVTWHYYLNGRTATRE 301
QY 309 DFLANDVDLFISSVQKLYQVYESTRRPKKVMLGFTSSAYGGAPLSDTFAAGFMWLDK 368
DB 302 DFLSSVDVLDLFISSVQKLYQVYESTRRPKKVMLGFTSSAYGGAPLSDTFAAGFMWLDK 361
QY 369 LGLSARMGIEVVMRQVFFGAGNYHLVDENFPLPDYWLSTLFKKLVGTVMASVQSGSR 428
DB 362 LGLSAQGLGIEVVMRQVFFGAGNYHLVDENFPLPDYWLSTLFKKLVGTVMASVQSGSR 421
QY 429 RKLRYVLIHCTNTDNPRYKEGDITLYALINLHNTYKTLRLPYPSNKQVQNYLLRPLGPHGL 488
DB 422 SKLRVYLHCTNTVHYHRYEGDITLYALINLHNTYKTLRLPYPSNKQVQNYLLRPLGPHGL 481
QY 489 LKRSVQNLGLTKMVDQDTLPLMEKPLRPGSSLGIPAFSVPFVIRNAKVAACI 543
DB 482 LKRSVQNLGLTKMVDQDTLPLMEKPLRPGSSLGIPAFSVPFVIRNAKVAACI 536
RESULT 7
QY09QZF8 PRELIMINARY; PRT; 536 AA.
AC Q90ZF8;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE Heparanase.
GN Name=Hep;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxId=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22194309; PubMed=12077130; DOI=10.1074/jbc.M203282200;
RA Podjma-Inoue K.A., Yokote H., Sakaguchi K., Ikuta M., Yanagishita M.,
RT "Characterization of heparanase from a rat parathyroid cell line."
RL J. Biol. Chem. 277.32459-32465 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RA Podjma K.A., Yokote H., Sakaguchi K., Ikuta M., Yanagishita M.,
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.

DR EMBL: AF184967; AA04563.1;
DR InterPro: IPR005199; Glyco_hydro_79N.
DR Pfam: PF03662; Glyco_hydro_79n; 1.
SQ SEQUENCE 536 AA; 60568 MW; 6208B1PD9EE28421 CRC64;
Query Match 74.7%; Score 2123; DB 2; Length 536;
Best Local Similarity 75.7%; Pred. No. 9.5e-151;
Matches 405; Conservative 51; Mismatches 79; Indels 0; Gaps 0;
QY 9 LPPMLLLGLPGLSPGALPPAQAQDVVDLDFPQEPHLVSPSPSLVTIDANLATD 68
DB 2 LRPLLLMKRLALVGTGTAAGTAPTKVDVLDLFTYKRLFGQSPSPSLSTIDASLATD 61
QY 69 PRFLILGSPKRLTLARGSPAYLRFGGKTDFLIPPKKESTFEERSYWGQVQNDICK 128
DB 62 PRFLTLGSPRLRLARGSPAYLRFGGKTDFLIPPKKESTFEERSYWGQVQNDICK 121
QY 129 YGSIIPDVEKRLLEMPYQOQLLRHNYQKKFKNSTYSSSDVLYTFANSGDLIFGL 188
DB 122 SERVSADVLRKIQEMWPFQELLLREOYQREPKNSTYSSSDVLYTFANSGDLIFGL 181
QY 189 NALLRTADLQNNSSNAQQLLDYCSSKGYNISWELGNEPNSFLKKADIFINGSOLGEDYIQ 248
DB 182 NALLRTADLQNNSSNAQQLLDYCSSKGYNISWELGNEPNSFLKKADIFINGSOLGEDYIQ 241
QY 249 LHKLLRKSTFKNAKLYGPDVQPRRKTAQMLKSLFKAGEVIDSVTWHYYLNGRTATRE 308
DB 242 LHKLLQKSAFQNAKLYGPDIGQPRGKTIVKLRSFLKAGEVIDSVTWHYYLNGRTATRE 301
QY 309 DFLANDVDLFISSVQKLYQVYESTRRPKKVMLGFTSSAYGGAPLSDTFAAGFMWLDK 368
DB 302 DFLSSVDVLDLFISSVQKLYQVYESTRRPKKVMLGFTSSAYGGAPLSDTFAAGFMWLDK 361
QY 369 LGLSARMGIEVVMRQVFFGAGNYHLVDENFPLPDYWLSTLFKKLVGTVMASVQSGSR 428
DB 362 LGLSAQGLGIEVVMRQVFFGAGNYHLVDENFPLPDYWLSTLFKKLVGTVMASVQSGSR 421
QY 429 RKLRYVLIHCTNTDNPRYKEGDITLYALINLHNTYKTLRLPYPSNKQVQNYLLRPLGPHGL 488
DB 422 SKLRVYLHCTNTVHYHRYEGDITLYALINLHNTYKTLRLPYPSNKQVQNYLLRPLGPHGL 481
QY 489 LKRSVQNLGLTKMVDQDTLPLMEKPLRPGSSLGIPAFSVPFVIRNAKVAACI 543
DB 482 LKRSVQNLGLTKMVDQDTLPLMEKPLRPGSSLGIPAFSVPFVIRNAKVAACI 536
RESULT 8
QY09YK5 PRELIMINARY; PRT; 523 AA.
AC Q90YK5;
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE Heparanase.
GN Gallus gallus (Chicken).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxId=9031;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21369599; PubMed=1187326; DOI=10.1074/jbc.M102462200;
RA Goldsmith O., Zcharia E., Aingorn H., Guatca-Rangini Z., Atzmon R.,
RA Michael I., Becker I., Mitrani E., Vlodavsky I.,
RT "Expression pattern and secretion of human and chicken heparanase are
determined by their signal peptide sequence."
RL J. Biol. Chem. 276.229178-229187(2001).
DR EMBL: AY037007; AAK82648.1;
DR Pfam: PF03662; Glyco_hydro_79n; 1.
SQ SEQUENCE 523 AA; 58386 MW; 8EB0B7B18C9BF881 CRC64;
Query Match 57.9%; Score 1645.5; DB 2; Length 523;
Best Local Similarity 60.2%; Pred. No. 6.8e-115;

RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
 RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
 RA Sasaki D., Shibata K., Shingawa A., Shiraki T., Sogabe Y., Tagami M.,
 RA Tagawa A., Takehashi F., Takaku-Akehira S., Takeda Y., Tanaka T.,
 RA Tomaru A., Toyota T., Yasunishi A., Muramatsu M., Hayashizaki Y.,
 RA Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
 RN
 RN SEQUENCE FROM N.A.
 RC STRAIN=JUL/J; Tissue=SpLenn;
 RA Huelt M.D., Wang J., Hornby J.R., Freeman C., Pagler E., McHenry J.,
 RA Parish C.R.,
 RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; A077467; AAL76083.1; -
 DR EMBL; AK040471; BAC30600.1; -
 DR EMBL; AF359507; AA015188.1; -
 DR MGD; MG1:1343124; Hspc.
 DR GO; GO:0005578; C:extracellular matrix (sensu Metazoa); TAS.
 DR InterPro; IPR005199; Glyco_hydro_79n; I.
 DR Pfam; PF03662; Glyco_hydro_79n; I.
 SQ SEQUENCE 535 AA; 60065 MW; 6E7A8302FB8A0DF CRC64;

Query Match 75.7%; Score 2150; DB 2; Length 535;
 Best Local Similarity 76.6%; Pred. No. 8.9e-153;
 Matches 407; Conservative 51; Mismatches 73; Indels 0; Gaps 0;

QY 13 LMLLLGRLPLSPGALPPRAQADVDLDFTOEPLHVSFSLSVITDANLATDPRFL 72
 DB 5 LLLMLGRLGALAAQAPAGTAPTDVVDLEFYTKRLRSVSPFSLITIDASLATDPRFL 64
 QY 73 ILGSPKRLTLARGSPAYLRFQGTCTDPLFDPKKESTFEERSYQWQOVNDICRYGSI 132
 DB 65 TFLGSPRLALARGSPAYLRFQGTCTDPLFDPKKESTFEERSYQWQOVNDICRYGSI 124
 QY 133 PDVEEKLRLLEMPYOEQLLREHYOKKFKNSTYSRSSVDVLYTFANCGLDLIFGINALL 192
 DB 125 SAAVLRKLQVEMPFQELLLREQYQKEFKNSTYSRSSVDMLYSFAKCSGLDLIFGINALL 184
 QY 193 RTADLQWNSNNAQLLDYSSKGYNISWELGNEPNSFLKKADI FINGSLGEDIYOLHKL 252
 DB 185 RPPDLRMNSNNAQLLDYSSKGYNISWELGNEPNSFWKKAHLLIDGLGDFVFLHKL 244
 QY 253 LRKSTFKNAKLYGPPVGOVRRRTAKMLKSFKAAGEVIDSVTHHHYLLNGRTATREDPLN 312
 DB 245 LORSAPQNAKLYGPPDGGPRGKTIVKLRSFLKAAGEVIDSLTWHHHYLLNGRTATKEDPLS 304
 QY 313 PVDLIFISSVQKVPQVVESTPRGKKVWLGETSSAYGAGAPLLSDTFAAGFMWLDKLGIS 372
 DB 305 SDVLDTFILSVQKILKVTKEITPGKKVWLGETSSAYGAGAPLLSNTFAAGFMWLDKLGIS 364
 QY 373 ARMGIEVVNRQVFPFAGNHYLVNDENFDPLPDYWLSLFFKLVGTKVLMAVSGSKRRKL 432
 DB 365 AQMGIEVVNRQVFPFAGNHYLVNDENFDPLPDYWLSLFFKLVGTKVLMAVSGSKRRKL 424
 QY 433 VYLHCTNTDNPYKKGDLTLVAINLHNTVKYRLPYPSFNKOVDKYLRLPGHGLSKS 492
 DB 425 VYLHCTNVNHPYKQGBDTLVYINLHNTVKYRLKVPPLPRKPVDTYLLKPSGPDGLSKS 484
 QY 493 VOLNGILTKMVDQTLPLMEKPLRPGSSGLPAPSYSPFVIRNAKVAACI 543
 DB 485 VOLNGILTKMVDQTLPLTEKPLRPGSGLSLPAPSYSPFVIRNAKVAACI 535

RESULT 5
 06Y6Z1 PRELIMINARY; PRT; 535 AA.
 AC 06Y6Z1;
 DT 05-JUL-2004 (TREMBlrel. 27, Created)
 DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
 DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
 DE Heparanase.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;
 RN
 RN SEQUENCE FROM N.A.
 RP Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
 RX MEDLINE=22841152; PubMed=12837765; DOI=10.1074/jbc.M300925200;
 RA Gong F., Jemth P., Galvis M.L.E., Vlodeavsky I., Horner A., Lindahl U.,
 RA Li J.P.,
 RT "Processing of macromolecular heparin by heparanase."
 RL J. Biol. Chem. 278:35152-35158(2003).
 RN
 RN SEQUENCE FROM N.A.
 RA Li J.-P., Gong F., Lindahl U.,
 RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY151051; AAN41636.1; -
 DR GO; GO:0005578; C:extracellular matrix (sensu Metazoa); TAS.
 DR InterPro; IPR005199; Glyco_hydro_79n; I.
 DR Pfam; PF03662; Glyco_hydro_79n; I.
 SQ SEQUENCE 535 AA; 59992 MW; 3748ABE3795C718A CRC64;

Query Match 75.3%; Score 2140; DB 2; Length 535;
 Best Local Similarity 76.6%; Pred. No. 5e-152;
 Matches 407; Conservative 50; Mismatches 74; Indels 0; Gaps 0;

QY 13 LMLLLGRLPLSPGALPPRAQADVDLDFTOEPLHVSFSLSVITDANLATDPRFL 72
 DB 5 LLLMLGRLGALAAQAPAGTAPTDVVDLEFYTKRLRSVSPFSLITIDASLATDPRFL 64
 QY 73 ILGSPKRLTLARGSPAYLRFQGTCTDPLFDPKKESTFEERSYQWQOVNDICRYGSI 132
 DB 65 TFLGSPRLALARGSPAYLRFQGTCTDPLFDPKKESTFEERSYQWQOVNDICRYGSI 124
 QY 133 PDVEEKLRLLEMPYOEQLLREHYOKKFKNSTYSRSSVDVLYTFANCGLDLIFGINALL 192
 DB 125 SAAVLRKLQVEMPFQELLLREQYQKEFKNSTYSRSSVDMLYSFAKCSGLDLIFGINALL 184
 QY 193 RTADLQWNSNNAQLLDYSSKGYNISWELGNEPNSFLKKADI FINGSLGEDIYOLHKL 252
 DB 185 RPPDLRMNSNNAQLLDYSSKGYNISWELGNEPNSFWKKAHLLIDGLGDFVFLHKL 244
 QY 253 LRKSTFKNAKLYGPPVGOVRRRTAKMLKSFKAAGEVIDSVTHHHYLLNGRTATREDPLN 312
 DB 245 LORSAPQNAKLYGPPDGGPRGKTIVKLRSFLKAAGEVIDSLTWHHHYLLNGRTATKEDPLS 304
 QY 313 PVDLIFISSVQKVPQVVESTPRGKKVWLGETSSAYGAGAPLLSDTFAAGFMWLDKLGIS 372
 DB 305 SDVLDTFILSVQKILKVTKEITPGKKVWLGETSSAYGAGAPLLSNTFAAGFMWLDKLGIS 364
 QY 373 ARMGIEVVNRQVFPFAGNHYLVNDENFDPLPDYWLSLFFKLVGTKVLMAVSGSKRRKL 432
 DB 365 AQMGIEVVNRQVFPFAGNHYLVNDENFDPLPDYWLSLFFKLVGTKVLMAVSGSKRRKL 424
 QY 433 VYLHCTNTDNPYKKGDLTLVAINLHNTVKYRLPYPSFNKOVDKYLRLPGHGLSKS 492
 DB 425 VYLHCTNVNHPYKQGBDTLVYINLHNTVKYRLKVPPLPRKPVDTYLLKPSGPDGLSKS 484
 QY 493 VOLNGILTKMVDQTLPLMEKPLRPGSSGLPAPSYSPFVIRNAKVAACI 543
 DB 485 VOLNGILTKMVDQTLPLTEKPLRPGSGLSLPAPSYSPFVIRNAKVAACI 535

RESULT 6
 071RP1 PRELIMINARY; PRT; 536 AA.
 AC 071RP1;
 DT 05-JUL-2004 (TREMBlrel. 27, Created)
 DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
 DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
 DE Heparanase.
 GN Name=Hspe;
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OC NCBI_TaxID=10116;
 RN [1]

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RESULT 3
ID 09MYO PRELIMINARY; PRT; 545 AA.
AC 09MYO
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Heparanase.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Placenta;
RX MEDLINE=21176669; PubMed=11277877;
RA Kizaki K., Nakano H., Nakano H., Takahashi T., Imai K., Hashizume K.;
RT "Expression of heparanase mRNA in bovine placenta during gestation.";
RL Reproduction 121:573-580(2001).
DR EMBL, AF281160; AAF87301.2;
DR InterPro, IPR005199; Glyco_Hydro_79N.
DR Pfam, PF03662; Glyco_Hydro_79n.1.
SQ SEQUENCE 545 AA; 61076 MW; FAC4BDFD855B933 CRC64;

Query Match 80.3%; Score 2282; DB 2; Length 545;
Best Local Similarity 79.8%; Pred. No. 1,1e-162;
Matches 435; Conservative 35; Mismatches 73; Indels 2; Gaps 1;

QY 1 MLRRKPPALPPMLL--LGLPLGLSPGALPPPAQADVDLDFTQSPHLVSPFLS 58
DB 1 MLACRKPGRPPPLLLPLGLGPCSPCTPAAPADAAELFPTTERPLHLVSPAFLS 60
QY 59 VTIDANLATDPPRLILSGPKRTIARGSPAYLRGGKTKTPIIFDPKKESTFEERSY 118
DB 61 FTIDANLATDPPRFPTFLGSSKRTIARGAPAYLRGGKNGDFLLFDPKKEPAFEERSY 120
QY 119 OSQVNDICKYSGIPDVEEKLRLWPYQEOQLLRHYQKFKFNSTYSSSDVLYTFAN 178
DB 121 LSQSNODICKSGSIPDVEEKLRLWPYQEOQLLRHYQKFKFNSTYSSSDVLYTFAS 180
QY 179 CSGLDLIFGLNALRLTADLQWNSNAQLLDYCSSKXNYISWELGNEPNSFLKADIFIN 238
DB 181 CGSLNLFEGVNLRLRTDMHMSNAQLLDYCSSKXNYISWELGNEPNSFORKAGIFIN 240
QY 239 GSQLEGDIYQLHKLKSTFKNAKLYGPVGGQPRKRTAKMLSGFLKAGGEVIDSYTMHY 298
DB 241 GROLGEDIYQLHKLKSTFKNAKLYGPVGGQPRKRTAKMLSGFLKAGGEVIDSYTMHY 300
QY 299 YNGRATREDPFLNPVDLIFITSSVQKVFQVVESTPRGKVMLGFTSSAYGGAPLLSDT 358
DB 301 YNGRATREDPFLNPVDLIFITSSVQKRIYKRIPLKVMLGFTSSAYGGAPLLSDT 360
QY 359 FAAGFWMLDLGLSARMGIEVVMRQVFGAGNYHLVDENFDPLDYMLLFEKLVGYTY 418
DB 361 FAAGFWMLDLGLSARMGIEVVMRQVFGAGNYHLVDENFDPLDYMLLFEKLVGYTY 420
QY 419 LMASVSGSKRKRIYVLIHCTNDNPRYKGGDLTVYINLANTKYLRLPFRPNKQVDXY 478
DB 421 LMASVSGSKRKRIYVLIHCTNDNPRYKGGDLTVYINLANTKYLRLPFRPNKQVDXY 480
QY 479 LRLPLPGHLLKSVYQNLGLTKMVDQTLPLMEKPLRPGSSILGPAFVSFFVIRNKK 538
DB 481 LRLPLPGHLLKSVYQNLGLTKMVDQTLPLMEKPLRPGSSILGPAFVSFFVIRNKK 540
QY 539 VAACT 543
DB 541 VAACT 545

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AC 08K3K3;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Heparanase (mus musculus 0 day neonate thymus cDNA, RIKEN full-length
DE enriched library, clone:A43010M94 product:heparanase, full insert
DE sequence).
GN Name=Hspe; Synonyms=Hpa, Hspe;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=FVB;
RA Miao H.-Q., Navarro E., Patel S., Sargent D., Koo H., Wan H.,
RA Plata A., Zhou Q., Ludwig D., Bohlen P., Kussie P.;
RT "Cloning, expression, and purification of mouse heparanase.";
RL Protein Expr. Purif. 0:0-0(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Thymus;
RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning.";
RL Meth. Enzymol. 303:19-44(1999).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Thymus;
RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA "RIKEN FANTOM Consortium";
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Thymus;
RA The FANTOM Consortium;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
RN [5]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Thymus;
RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Kono H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subcloning of cap-trapper-selected cDNAs to
RT prepare full-length cDNA libraries for rapid discovery of new genes.";
RL Genome Res. 10:1617-1630(2000).
RN [6]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Thymus;
RX MEDLINE=20530913; PubMed=11076661; DOI=10.1101/gr.152600;
RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Saeki N., Carninci P.,
RA Kono H., Akiyama J., Nishi K., Kitsuina T., Taishiro H., Itoh M.,
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishino T., Harada A.,
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashwagi K.,
RA Fujitake S., Inoue K., Togawa Y., Izawa M., Ohara E., Matsuda M.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format
RT sequencing pipeline with 384 multichannel sequencer.";
RL Genome Res. 10:1757-1771(2000).
RN [7]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Thymus;
RA Adachi J., Aizawa K., Akimura T., Arikawa T., Bono H., Carninci P.,
RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
RA Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
RA Katoh H., Kawai J., Kojima Y., Kondo S., Kono H., Kouda M., Koya S.,
RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,

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RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywinski M.I., Skalek U., Smailus D.E., Schermer A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 RN
 RP SEQUENCE FROM N.A.
 RC TISSUE=pancreas;
 RA Strausberg R.;
 RL Submitted (Apr-2003) to the EMBL/GenBank/DBJ databases.
 RN
 RP SEQUENCE FROM N.A.
 RA Vlodavsky I., Friedman Y., Elkin M., Aingorn H., Aramon R.,
 RA Ishai-Michaeli R., Bitan M., Pappo O., Peretz T., Michael I.,
 RA Spector L., Becker I.;
 RL Submitted (Apr-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF165154; AAD45379.1; -;
 DR EMBL; AF152376; AAD45669.1; -;
 DR EMBL; AF155510; AAD54941.1; -;
 DR EMBL; BC051321; AAH51321.1; -;
 DR EMBL; AF144325; AAD41342.1; -;
 DR GO; GO:0004566; F-beta-glucuronidase activity; TAS.
 DR GO; GO:0006029; P-glycoprotein-mediated transport; TAS.
 DR InterPro; IPR005199; Glyco_hydro_79N.
 DR Pfam; PF03662; Glyco_hydro_79n; 1.
 FT CHAIN 158 543 heparanase.
 SQ SEQUENCE 543 AA; 61176 MW; AD262EC267334AB2 CRC64;

Query Match 99.9%; Score 2838; DB 2; Length 543;
 Best Local Similarity 99.8%; Pred. No. 1.9e-204;
 Matches 542; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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 QY 61 IDANLATDPRFLLILGSPKRLTARGLSPAYLRFGGTKTDPLFPDKKESTFEERSY 120
 DB 61 IDANLATDPRFLLILGSPKRLTARGLSPAYLRFGGTKTDPLFPDKKESTFEERSY 120
 QY 121 QVNODICKYGSIPPDVEEKLRLMPYQEOQLLREHYOKKPKNSTYSSSDVLYTFAN 180
 DB 121 QVNODICKYGSIPPDVEEKLRLMPYQEOQLLREHYOKKPKNSTYSSSDVLYTFAN 180
 QY 181 GDDLIFGLNALRTADLQWSSNAQLLDYCSSKGNISWELGNENPSFLKADIFIN 240
 DB 181 GDDLIFGLNALRTADLQWSSNAQLLDYCSSKGNISWELGNENPSFLKADIFIN 240
 QY 241 QGGEVDYIQLHKLRLKSTFFKNAKLYGPDVGPARRKTAAMLKSPFKAGGEVIDSVTWHY 300
 DB 241 QGGEVDYIQLHKLRLKSTFFKNAKLYGPDVGPARRKTAAMLKSPFKAGGEVIDSVTWHY 300
 QY 301 NGRTATREDPLNDVDLDFISSVQKFPQVESRPGKWLGETSSAYGGAPLSDTFA 360
 DB 301 NGRTATREDPLNDVDLDFISSVQKFPQVESRPGKWLGETSSAYGGAPLSDTFA 360
 QY 361 AGFMWLDKLGISARMGIEVVMROVFFGAGNYHLVDENFDPDLDPYWSLFLFKLVGTXY 420
 DB 361 AGFMWLDKLGISARMGIEVVMROVFFGAGNYHLVDENFDPDLDPYWSLFLFKLVGTXY 420
 QY 421 ASVQSGSKRRKRLRYLHCTNTDNPRIYEGDLTLVAINLHNTKYLRLPYPSNKOVDKY 480
 DB 421 ASVQSGSKRRKRLRYLHCTNTDNPRIYEGDLTLVAINLHNTKYLRLPYPSNKOVDKY 480
 QY 481 RPLGPHGLSKSVQNLGLTLKAVDDQTLPLMEKPLRPGSSLGLPASYSFPVIRNAKY 540
 DB 481 RPLGPHGLSKSVQNLGLTLKAVDDQTLPLMEKPLRPGSSLGLPASYSFPVIRNAKY 540
 QY 541 ACI 543
 DB 541 ACI 543

RESULT 2
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 ID Q9UL39 PRELIMINARY; PRT; 545 AA.
 AC Q9UL39;
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
 DE Heparanase.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_Taxid=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Placenta;
 RX MEDLINE=20229546; PubMed=10764835; DOI=10.1093/glycob/10.5.467;
 RA Dempsey L.A., Plummer T.B., Coombes S.L., Platt J.U.;
 RT "Heparanase expression in invasive trophoblasts and acute vascular
 RT damage.";
 RL Glycobiology 10:467-475(2000).
 DR EMBL; AF084467; AAD54516.1; -;
 DR Genew; HGNC:5164; HSE.
 DR InterPro; IPR005199; Glyco_hydro_79N.
 DR Pfam; PF03662; Glyco_hydro_79n; 1.
 SQ SEQUENCE 545 AA; 61417 MW; 67B80ACD73C5A9A1 CRC64;

Query Match 99.1%; Score 2817; DB 2; Length 545;
 Best Local Similarity 99.4%; Pred. No. 7.1e-203;
 Matches 542; Conservative 1; Mismatches 0; Indels 2; Gaps 2;

QY 1 MLRRKPPALPPMLLLGLPLSGALPPRQAQDVVDLDFPQEPHLVSPSLSTT 58
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 QY 59 VTIDANLATDPRFLLILGSPKRLTARGLSPAYLRFGGTKTDPLFPDKKESTFEERSY 118
 DB 61 VTIDANLATDPRFLLILGSPKRLTARGLSPAYLRFGGTKTDPLFPDKKESTFEERSY 120
 QY 119 QVNODICKYGSIPPDVEEKLRLMPYQEOQLLREHYOKKPKNSTYSSSDVLYTFAN 178
 DB 121 QVNODICKYGSIPPDVEEKLRLMPYQEOQLLREHYOKKPKNSTYSSSDVLYTFAN 180
 QY 179 GDDLIFGLNALRTADLQWSSNAQLLDYCSSKGNISWELGNENPSFLKADIFIN 238
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 QY 239 GSQGEVDYIQLHKLRLKSTFFKNAKLYGPDVGPARRKTAAMLKSPFKAGGEVIDSVTWHY 298
 DB 241 GSQGEVDYIQLHKLRLKSTFFKNAKLYGPDVGPARRKTAAMLKSPFKAGGEVIDSVTWHY 300
 QY 299 YNGRTATREDPLNDVDLDFISSVQKFPQVESRPGKWLGETSSAYGGAPLSDTFA 358
 DB 301 YNGRTATREDPLNDVDLDFISSVQKFPQVESRPGKWLGETSSAYGGAPLSDTFA 360
 QY 359 PAAGFMWLDKLGISARMGIEVVMROVFFGAGNYHLVDENFDPDLDPYWSLFLFKLVGTXY 418
 DB 361 PAAGFMWLDKLGISARMGIEVVMROVFFGAGNYHLVDENFDPDLDPYWSLFLFKLVGTXY 420
 QY 419 LMASVQSGSKRRKRLRYLHCTNTDNPRIYEGDLTLVAINLHNTKYLRLPYPSNKOVDKY 478
 DB 421 LMASVQSGSKRRKRLRYLHCTNTDNPRIYEGDLTLVAINLHNTKYLRLPYPSNKOVDKY 480
 QY 479 LRPGLPHGLSKSVQNLGLTLKAVDDQTLPLMEKPLRPGSSLGLPASYSFPVIRNAKY 538
 DB 481 LRPGLPHGLSKSVQNLGLTLKAVDDQTLPLMEKPLRPGSSLGLPASYSFPVIRNAKY 540
 QY 539 VAACT 543
 DB 541 VAACT 545

091159207

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 23, 2005, 11:18:07 ; Search time 109.5 Seconds
(without alignments)
2539.352 Million cell updates/sec

Title: SEQ2A
Perfect score: 2842
Sequence: 1 MLRSKPLPPLMLLGP.....LPFSYSPFVIRNAVAACI 543

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: uniprot_03:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2838	99.9	543	2	Q9Y251 homo sapien
2	2817	99.1	545	2	Q9UJ39
3	2282	80.3	545	2	Q9MYV0 bos taurus
4	2150	75.7	535	2	Q8K3K3 mus musculu
5	2140	75.3	535	2	Q6VGT1 mus musculu
6	2135	75.1	536	2	Q71RPI rattus norv
7	2133	74.7	536	2	Q9QZF8
8	1645.5	57.9	523	2	Q90YK5 gallus gall
9	1154.5	40.6	592	2	Q9HB37
10	1146.5	40.3	592	2	Q8WMQ2
11	1015.5	35.7	548	2	Q8WMQ1
12	936.5	33.0	534	2	Q9HB38
13	897.5	31.6	480	2	Q9HB39
14	696	24.5	515	2	Q8T108
15	416	14.6	521	2	Q9SDA1
16	416	14.6	543	2	Q9F10
17	404	14.2	559	2	Q89F99
18	392.5	13.8	544	2	Q8H615
19	381	13.4	527	2	Q91C8
20	379	13.3	541	2	Q691I6
21	364	12.8	537	2	Q70YJ3
22	363	12.8	536	2	Q9FZP1
23	352.5	12.4	516	2	Q9F1K8
24	352.5	12.4	539	2	Q8L608
25	350.5	12.3	529	2	Q6Z0E2
26	169.5	6.0	190	2	Q82604
27	160	5.6	935	2	Q9VE79
28	141	5.0	559	2	Q7SFB0
29	136.5	4.8	463	2	Q63T97
30	130.5	4.6	493	2	Q9HK01
31	122.5	4.3	408	2	Q9HE21

32	122.5	4.3	408	2	Q9HE22	Q9he22 phanerochae
33	116.5	4.1	617	2	Q40996	Q40996 meales vir
34	114.5	4.0	1169	2	Q869K5	Q869K5 dictyostell
35	114	4.0	398	2	Q72RP7	Q72RP7 leptospira
36	114	4.0	398	2	Q8F410	Q8F410 leptospira
37	113.5	4.0	617	2	Q83295	Q83295 meales vir
38	113.5	4.0	1829	2	Q9KH44	Q9KH44 paracoa egg
39	113	4.0	390	2	Q8TPH7	Q8TPH7 methanococ
40	112.5	4.0	356	1	Y670_METUA	Y670_METUA methanococ
41	112.5	4.0	617	2	Q83647	Q83647 meales vir
42	112	3.9	732	2	Q7MSD4	Q7MSD4 wolfinella s
43	111.5	3.9	575	2	Q979W0	Q979W0 thermoplasma
44	111.5	3.9	575	2	Q43855	Q43855 vicia faba
45	111.5	3.9	617	2	Q40991	Q40991 meales vir

ALIGNMENTS

RESULT 1	Q9Y251	PRELIMINARY;	PRT;	543 AA.
ID	Q9Y251			
AC	Q9Y251;			
DT	01-NOV-1999 (TREMBLrel. 12, Created)			
DT	01-NOV-1999 (TREMBLrel. 12, Last sequence update)			
DT	25-OCT-2004 (TREMBLrel. 28, Last annotation update)			
DE	Heparanase.			
GN	Name=HPA; Synonyms=HPSE;			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.			
OX	NCBI_TaxID=9606;			
RP	SEQUENCE FROM N.A.			
RC	TISUE=Placenta;			
RX	MEDLINE=99321249; PubMed=10395326;			
RA	Hulec M.D., Freeman C., Hamdorf B.J., Baker R.T., Harris M.J.,			
RA	Parish C.R.;			
RT	"Cloning of mammalian heparanase, an important enzyme in tumor			
RT	invasion and metastasis";			
RL	Nat. Med. 5:803-809(1999).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RC	TISUE=Placenta;			
RX	MEDLINE=99335379; PubMed=10405343; DOI=10.1006/dbrc.1999.0962;			
RA	Kussie P.H., Hulmes J.D., Ludwig D.L., Patel S., Navarro E.C.,			
RA	Seddon A.P., Giorgio N.A., Bohlen P.;			
RT	"Cloning and functional expression of a human heparanase gene";			
RL	Biochem. Biophys. Res. Commun. 261:183-187(1999).			
RN	[3]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=9937052; PubMed=10446189; DOI=10.1074/jbc.274.34.24153;			
RA	Toyoshima M., Nakajima M.;			
RT	"Human heparanase. Purification, characterization, cloning, and			
RT	expression";			
RL	J. Biol. Chem. 274:24153-24160(1999).			
RN	[4]			
RP	SEQUENCE FROM N.A.			
RC	TISUE=Pancreas;			
RX	MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;			
RA	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,			
RA	Klausner R.D., Collins J.S., Wagner L., Shennan C.M., Schuler G.D.,			
RA	Altschul S.F., Zeeberg B., Buettow K.H., Schaefer C.F., Bhat N.K.,			
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heish F.,			
RA	Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,			
RA	Scapleton M., Soares M.B., Bonaldo W.F., Casavant J.L., Scheetz T.E.,			
RA	Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Pange C.,			
RA	Raha S.S., Loughellano N.A., Peters G.J., Abramson R.D., Miliady S.J.,			
RA	Bosak S.A., McMan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,			
RA	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,			
RA	Villalon D.K., Murny D.M., Sodergren E.J., Lu X., Gibbs R.A.,			
RA	Faney J., Heiton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,			
RA	Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,			

Protein Sequence Searches - February 2005

All of the sequence databases on ABSS have recently been updated.

- Please note that the curators of the UniProt database have purged some temporary accession numbers from the most recent version of UniProt. These sequences have been assigned new permanent accession numbers. The new UniProt record may not contain the previous temporary accession number.
- If you encounter an accession number from an older search run against UniProt (results file extension **.rup**) that can no longer be found in the database, the permanent record with the new accession number can be found by searching the old accession number in the UniProt Protein Archive database (UniPARC) at:

<http://www.pir.uniprot.org/database/archive.shtml>

If you have any questions regarding this information or your results, please contact any STIC searcher.

When submitting sequence search results for scanning into IFW, please include a copy of this attachment to assist any future Examiners or members of the public who may encounter UniProt temporary accession numbers.

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